GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 14, 2004, 16:35:49 ; Search time 39 Seconds
(without alignments)
550.134 Million cell updates/sec

Title: US-10-623-629-2
Perfect score: 379
Sequence: 1 MKVLLLFAVFFCLVQRNSGD.....GDICSDPWNRCCVSSSIKNR 68

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	379	100.0	68	11	Q8VBV2	Q8vbv2 rattus norv
2	341	90.0	69	11	Q8K4N2	Q8k4n2 mus musculu
3	291	76.8	80	6	Q8SQD3	Q8sqd3 macaca mula
4	286	75.5	80	4	Q9H4P9	Q9h4p9 homo sapien
5	276	72.8	80	6	Q9MZ26	Q9mz26 pan troglod
6	228	60.2	82	6	Q8SQC5	Q8sqc5 macaca mula
7	75	19.8	64	6	O97942	O97942 capra hircu
8	75	19.8	67	11	Q7TNV9	Q7tnv9 mus musculu
9	71	18.7	29	6	Q8SQD5	Q8sqd5 macaca mula
10	69	18.2	341	11	Q80UP9	Q80up9 mus musculu
11	68	17.9	64	6	Q7YS43	Q7ys43 bubalus bub
12	66	17.4	64	6	Q95JD2	Q95jd2 pan troglod
13	66	17.4	729	10	Q8LMU8	Q8lmu8 oryza sativ
14	65.5	17.3	96	6	Q9TU00	Q9tu00 macaca mula
15	65.5	17.3	96	6	Q9TTZ9	Q9ttz9 macaca mula
16	65.5	17.3	96	6	P82318	P82318 macaca mula
17	65.5	17.3	1319	4	Q9HCD3	Q9hcd3 homo sapien
18	65	17.2	101	16	Q81KL6	Q81kl6 bacillus an
19	64.5	17.0	276	4	Q9Y417	Q9y417 homo sapien
20	64.5	17.0	375	16	Q8E982	Q8e982 shewanella
21	64	16.9	200	4	Q96Q79	Q96q79 homo sapien
22	64	16.9	233	4	Q9BU32	Q9bu32 homo sapien
23	64	16.9	239	4	Q96NT3	Q96nt3 homo sapien
24	63.5	16.8	67	11	Q8R2I6	Q8r2i6 mus musculu
25	63	16.6	139	5	Q19698	Q19698 caenorhabdi
26	63	16.6	148	13	Q90XI6	Q90xi6 amia calva
27	63	16.6	211	11	Q8BLZ0	Q8blz0 mus musculu
28	63	16.6	242	11	Q8BZI6	Q8bzi6 mus musculu
29	63	16.6	281	11	Q80XN8	Q80xn8 mus musculu
30	62.5	16.5	358	5	Q9U362	Q9u362 caenorhabdi
31	62.5	16.5	393	11	Q80VA4	Q80va4 mus musculu
32	62.5	16.5	685	11	Q8K0I3	Q8k0i3 mus musculu
33	62.5	16.5	837	11	Q80TK2	Q80tk2 mus musculu
34	62.5	16.5	909	11	Q8R5K2	Q8r5k2 mus musculu
35	62.5	16.5	956	11	Q99K22	Q99k22 mus musculu
36	62	16.4	139	5	O76358	O76358 caenorhabdi
37	62	16.4	205	16	O31812	O31812 bacillus su
38	61	16.1	112	10	Q8H286	Q8h286 ananas como
39	61	16.1	4706	10	Q9FN44	Q9fn44 arabidopsis
40	60.5	16.0	364	11	Q80ZM9	Q80zm9 mus musculu
41	60.5	16.0	365	4	Q8N2E5	Q8n2e5 homo sapien
42	60	15.8	101	16	Q816T9	Q816t9 bacillus ce
43	59.5	15.7	150	11	Q8VD85	Q8vd85 rattus tiom
44	59	15.6	644	16	O86346	O86346 mycobacteri
45	59	15.6	644	16	Q7U0Z6	Q7u0z6 mycobacteri

ALIGNMENTS

RESULT 1
Q8VBV2
ID Q8VBV2 PRELIMINARY; PRT; 68 AA.
AC Q8VBV2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Anti-microbial-like protein BIN-1B.
GN BIN-1B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Caput epididymis;
RA Li P., Shang Q., Zhang Y.D., Zhang Y.L.;
RT "Genomic DNA cloning of a rat epididymis-specific gene (Bin-1b).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Caput epididymis;
RA Li P., He B., Zhang Y.D., Zhang Y.L.;
RT "Cloning and characterization of a rat epididymis caput region-
RT specific cDNA (Bin-1b).";
RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF217089; AAL55637.1; -.
DR EMBL; AF217088; AAL55636.1; -.
SQ SEQUENCE 68 AA; 7799 MW; 86BBCC7A5D2FA53E CRC64;

Query Match 100.0%; Score 379; DB 11; Length 68;
Best Local Similarity 100.0%; Pred. No. 2e-44;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKVLLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
Db 1 MKVLLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60

Qy 61 VSSSIKNR 68

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                ||||||||
Db          61 VSSSIKNR 68


RESULT 2
Q8K4N2
ID   Q8K4N2      PRELIMINARY;      PRT;    69 AA.
AC   Q8K4N2;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   EP2e (ANTI-microbial-like protein BIN-1B homolog).
GN   9230111C08RIK OR MEP2E.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Epididymis;
RX   MEDLINE=22181517; PubMed=12193721;
RA   Yamaguchi Y., Nagase T., Makita R., Fukuhara S., Tomita T.,
RA   Tominaga T., Kurihara H., Ouchi Y.;
RT   "Identification of Multiple Novel Epididymis-Specific beta-Defensin
RT   Isoforms in Humans and Mice.";
RL   J. Immunol. 169:2516-2523(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Epididymis;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AB089183; BAC10633.1; -.
DR   EMBL; AK020333; BAC25623.1; -.
DR   MGD; MGI:1925378; 9230111C08Rik.
SQ   SEQUENCE   69 AA;  7901 MW;  635BB5249FF84F49 CRC64;

  Query Match             90.0%;  Score 341;  DB 11;  Length 69;
  Best Local Similarity   88.2%;  Pred. No. 3.4e-39;
  Matches   60;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 MKVLLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              ||||||||||||  || ||||||||||||||| ||:|||||||||||||||||||||||||
Db          1 MKVLLLFAVFFCFVQGNSGDIPPGIRNTVCLMQQGHCRLFMCRSGERKGDICSDPWNRCC 60

Qy         61 VSSSIKNR 68
                 |  |:|:|
Db         61 VPYSVKDR 68


RESULT 3
Q8SQD3
ID   Q8SQD3      PRELIMINARY;      PRT;    80 AA.
AC   Q8SQD3;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   EP2E protein.
GN   EP2.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Frohlich O., Po C., Young L.G.;
RT   "EP2 splicing variants in the rhesus monkey epididymis.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF466348; AAL74198.1; -.
SQ   SEQUENCE   80 AA;  9144 MW;  F85776E60130AF98 CRC64;

  Query Match             76.8%;  Score 291;  DB 6;  Length 80;
  Best Local Similarity   77.8%;  Pred. No. 3e-32;
  Matches   49;  Conservative    6;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 MKVLLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              |||  |||| |||||:|||||:|||||||:| ||:| |||| | |||:| ||||||||||
Db          1 MKVFFLFAVLFCLVRRNSGDVPPGIRNTICLMQQGTCRLFFCHSGEKKRDICSDPWNRCC 60

Qy         61 VSS 63
                ||:
Db         61 VSN 63


RESULT 4
Q9H4P9
ID   Q9H4P9      PRELIMINARY;      PRT;    80 AA.
AC   Q9H4P9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   EP2E.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Frohlich O., Po C., Young L.G.;
RT   "Genomic organization of the human epididymal EP2 gene and its
RT   relationship to defensin genes.";
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY005129; AAG21882.1; -.
SQ   SEQUENCE   80 AA;  9091 MW;  CF3DE98570684019 CRC64;

  Query Match             75.5%;  Score 286;  DB 4;  Length 80;
  Best Local Similarity   76.6%;  Pred. No. 1.5e-31;
  Matches   49;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 MKVLLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              |||  |||| ||||| ||||:||||||:| ||:| |||| | |||:| ||||||||||
Db          1 MKVFFLFAVLFCLVQTNSGDVPPGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCC 60

Qy         61 VSSS 64
                ||::
Db         61 VSNT 64


RESULT 5
Q9MZ26
ID   Q9MZ26      PRELIMINARY;      PRT;    80 AA.
AC   Q9MZ26;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   EP2 protein variant E.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20277601; PubMed=10819450;
RA   Frohlich O., Po C., Murphy T., Young L.G.;
RT   "Multiple promoter and splicing mRNA variants of the epididymis-
RT   specific gene EP2.";
RL   J. Androl. 21:421-430(2000).
DR   EMBL; AF263555; AAF87722.1; -.
SQ   SEQUENCE   80 AA;  9107 MW;  CF21F5856C744019 CRC64;

  Query Match             72.8%;  Score 276;  DB 6;  Length 80;
  Best Local Similarity   75.0%;  Pred. No. 3.5e-30;
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  Matches   48;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MKVLLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              |||  |||| ||||| ||||:| |||||:| ||:| |||| | |||:| ||||||||||
Db          1 MKVFFLFAVLFCLVQTNSGDVPLGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCC 60

Qy         61 VSSS 64
              ||::
Db         61 VSNT 64


RESULT 6
Q8SQC5
ID   Q8SQC5      PRELIMINARY;      PRT;    82 AA.
AC   Q8SQC5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   EP2Q protein.
GN   EP2.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Frohlich O., Po C., Young L.G.;
RT   "EP2 splicing variants in the rhesus monkey epididymis.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF466356; AAL74206.1; -.
DR   InterPro; IPR007988; Sperm_Ag_HE2.
DR   Pfam; PF05324; Sperm_Ag_HE2; 1.
SQ   SEQUENCE   82 AA;  9329 MW;  B063D35530886314 CRC64;

  Query Match             60.2%;  Score 228;  DB 6;  Length 82;
  Best Local Similarity   66.7%;  Pred. No. 1.4e-23;
  Matches   40;  Conservative    6;  Mismatches    8;  Indels    6;  Gaps    1;

Qy          4 LLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSS 63
              ||| |: |      ||:|||||||:| ||:| |||| | |||:| ||||||||||||:
Db         12 LLLVALLF------PGDVPPGIRNTICLMQQGTCRLFFCHSGEKKRDICSDPWNRCCVSN 65


RESULT 7
O97942
ID   O97942      PRELIMINARY;      PRT;    64 AA.
AC   O97942;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta defensin-2 precursor.
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20002622; PubMed=10531296;
RA   Zhao C., Nguyen T., Liu L., Shamova O., Brogden K., Lehrer R.I.;
RT   "Differential expression of caprine beta-defensins in digestive and
RT   respiratory tissues.";
RL   Infect. Immun. 67:6221-6224(1999).
DR   EMBL; AJ009877; CAA08905.1; -.
DR   HSSP; P46170; 1BNB.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0003795; F:antimicrobial peptide activity; IEA.
DR   GO; GO:0006952; P:defense response; IEA.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Signal.
FT   SIGNAL        1     26       POTENTIAL.
FT   CHAIN        27     64       BETA DEFENSIN-2.
SQ   SEQUENCE   64 AA;  7165 MW;  8672F55D9BF800BA CRC64;

  Query Match             19.8%;  Score 75;  DB 6;  Length 64;
  Best Local Similarity   30.4%;  Pred. No. 0.012;
  Matches   17;  Conservative    8;  Mismatches   31;  Indels    0;  Gaps    0;

Qy          5 LLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              || |:|| ::    ||     | :  |:  :| |     |     |:   |  |  :||
Db          6 LLLALFFLVLSAGSGFTQGIINHRSCYRNKGVCAPARCPRNMRQIGTCHGPPVKCC 61


RESULT 8
Q7TNV9
ID   Q7TNV9      PRELIMINARY;      PRT;    67 AA.
AC   Q7TNV9;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Beta defensin 14.
GN   DEFB14.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57Bl/6;
RA   Maxwell A.;
RT   "Amino acid residues subject to positive selection in murine b-
RT   defensin antimicrobial peptides.";
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57Bl/6;
RA   Dorin J.R.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ578468; CAE17665.2; -.
SQ   SEQUENCE   67 AA;  7718 MW;  EEFF0D93ADF17452 CRC64;

  Query Match             19.8%;  Score 75;  DB 11;  Length 67;
  Best Local Similarity   24.1%;  Pred. No. 0.013;
  Matches   14;  Conservative   12;  Mismatches   32;  Indels    0;  Gaps    0;

Qy          3 VLLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              :| :| : | :        :|  :|   | :: | | :  |   |  :   ||:   :||
Db          6 LLFVFLILFLVPAPGDAFLPKTLRKFFCRIRGGRCAVLNCLGKEEQIGRCSNSGRKCC 63


RESULT 9
Q8SQD5
ID   Q8SQD5      PRELIMINARY;      PRT;    29 AA.
AC   Q8SQD5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   EP2B protein.
GN   EP2.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Frohlich O., Po C., Young L.G.;
RT   "EP2 splicing variants in the rhesus monkey epididymis.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF466346; AAL74196.1; -.
SQ   SEQUENCE   29 AA;  3403 MW;  0D8ADC21B61FC425 CRC64;
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  Query Match             18.7%;  Score 71;  DB 6;  Length 29;
  Best Local Similarity   77.8%;  Pred. No. 0.019;
  Matches   14;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MKVLLLFAVFFCLVQRNS 18
              |||  |||| ||||:|||
Db          1 MKVFFLFAVLFCLVRRNS 18
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RESULT 10
Q80UP9
ID   Q80UP9      PRELIMINARY;      PRT;   341 AA.
AC   Q80UP9;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   LOC216790 protein (Fragment).
GN   LOC216790.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CZECH II; TISSUE=Breast tumor;
RA   Strausberg R.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC046431; AAH46431.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00069; pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   341 AA;  38078 MW;  63BDB2E3FFD71914 CRC64;
```

```
  Query Match             18.2%;  Score 69;  DB 11;  Length 341;
  Best Local Similarity   28.8%;  Pred. No. 0.45;
  Matches   17;  Conservative   11;  Mismatches   21;  Indels   10;  Gaps    2;

Qy         18 SGDIP---PGIRNTVCFMQRGHCRLFMCRSGERKG-------DICSDPWNRCCVSSSIK 66
               ||: |    | |:    :::|  ||  | :|  |         :|: || | | |: ::
Db        235 SGEYPESSEGTRDLQKGLRKGLIRLSRCYAGLSGGAVAFLQSSLCAQPWGRPCASTCLQ 293
```

```
RESULT 11
Q7YS43
ID   Q7YS43      PRELIMINARY;      PRT;    64 AA.
AC   Q7YS43;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Enteric beta defensin preproprotein.
OS   Bubalus bubalis (Domestic water buffalo).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bubalus.
OX   NCBI_TaxID=89462;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Das D.K., Kumar A.;
RT   "Cloning and Characterization of Enteric Beta Defensin (EBD) cDNA in
RT   Buffalo (Bubalus bubalis).";
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY301005; AAP57565.1; -.
SQ   SEQUENCE   64 AA;  7054 MW;  498E9399816C005E CRC64;

  Query Match             17.9%;  Score 68;  DB 6;  Length 64;
  Best Local Similarity   31.6%;  Pred. No. 0.11;
  Matches   18;  Conservative    7;  Mismatches   30;  Indels    2;  Gaps    2;

Qy          5 LLFAVFFCLVQRNSGDIPPGIRN-TVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              || |: | ::   ||    |:||   |  :| |    |    |:   |  |  :||
Db          6 LLLALLFLVLSAGSG-FTQGVRNPQSCHRNKGICVPIRCPGNMRQIGTCLGPPVKCC 61
```

```
RESULT 12
Q95JD2
ID   Q95JD2      PRELIMINARY;      PRT;    64 AA.
AC   Q95JD2;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Beta-defensin-3 (Fragment).
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin;
RA   Duits L.A., Langermans J.A.M., Ravensbergen B., Paltansing S.,
RA   Vervenne R.A.W., Hiemstra P.S., Thomas A.W., Nibbering P.H.;
RT   "Expression of chimpanzee (Pan troglodytes) beta-defensin-3.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY033883; AAK61549.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0003795; F:antimicrobial peptide activity; IEA.
DR   GO; GO:0006952; P:defense response; IEA.
DR   InterPro; IPR001855; Defensin_beta.
DR   Pfam; PF00711; Defensin_beta; 1.
FT   NON_TER      64      64
SQ   SEQUENCE   64 AA;  7299 MW;  01C90D4B60218DC8 CRC64;

  Query Match             17.4%;  Score 66;  DB 6;  Length 64;
  Best Local Similarity   31.7%;  Pred. No. 0.21;
  Matches   19;  Conservative    8;  Mismatches   27;  Indels    6;  Gaps    2;

Qy          5 LLFAVFFCLVQRNSGDIPPGIRNTV----CFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              ||||: |  :   |   || ||:   | :: | | :  |  | :   ||    :||
Db          6 LLFALLFLFLVPVPGH--GGIINTLQKYYCRVRGGRCAVLTCLPKEEQIGKCSTRGRKCC 63
```

```
RESULT 13
Q8LMU8
ID   Q8LMU8      PRELIMINARY;      PRT;   729 AA.
AC   Q8LMU8;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   OSJNBA0040E17.32.
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RA   Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA   Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
RA   Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
RA   Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA   Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT   "Oryza sativa chromosome 10 BAC OSJNBa0040E17 genomic sequence.";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RA   The Rice Chromosome 10 Sequencing Consortium;
RT   "In-depth view of structure, activity, and evolution of rice
RT   chromosome 10.";
RL   Science 300:1566-1569(2003).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RA   Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC097278; AAM93469.1; -.
DR   EMBL; AE017067; AAP52549.1; -.
DR   Gramene; Q8LMU8; -.
DR   InterPro; IPR007658; DUF594.
DR   Pfam; PF04578; DUF594; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   729 AA;  82584 MW;  8FFC11F6C675783A CRC64;

  Query Match             17.4%;  Score 66;  DB 10;  Length 729;
  Best Local Similarity   28.8%;  Pred. No. 2.5;
  Matches   19;  Conservative   12;  Mismatches   25;  Indels   10;  Gaps    4;

Qy          2 KVLLLFAVFFCLVQRNSGDIPPGIRNTV----CFMQRGHCRLFMCRSGERKGDICSDP-- 55
              :||  : :|  :|: |   :|   |: :    |    ||||  |   ||:   : : |
Db        489 EVLSNYMMFLLVVKPNM--LPGAARHNIHLPSCEQIEGHCR--MGFGGEKDNPVAASPIS 544

Qy         56 WNRCCV 61
                ||  |:
Db        545 WNPYCM 550


RESULT 14
Q9TU00
ID   Q9TU00      PRELIMINARY;      PRT;    96 AA.
AC   Q9TU00;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Alpha-defensin 1.
GN   MNP1.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhao C., Nguyen T., Lehrer R.I.;
RT   "cDNA cloning of three alpha-defensins and three demidefensins from
RT   rhesus monkey bone marrow.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF184159; AAF07925.1; -.
DR   HSSP; P11479; 1DFN.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0003795; F:antimicrobial peptide activity; IEA.
DR   GO; GO:0006952; P:defense response; IEA.
DR   InterPro; IPR006081; Defensin_alpha.
DR   InterPro; IPR006080; Defensin_mammal.
DR   InterPro; IPR002366; Defensin_propep.
DR   Pfam; PF00323; defensins; 1.
DR   Pfam; PF00879; Defensin_propep; 1.
DR   SMART; SM00048; DEFSN; 1.
DR   PROSITE; PS00269; DEFENSIN; 1.
SQ   SEQUENCE   96 AA;  10534 MW;  A473B80CBFF575A2 CRC64;

  Query Match             17.3%;  Score 65.5;  DB 6;  Length 96;
  Best Local Similarity   35.6%;  Pred. No. 0.38;
  Matches   16;  Conservative    5;  Mismatches   15;  Indels    9;  Gaps    3;

Qy         20 DIPPGIR-NTVCFMQRGHCRLFMCRSGERKGDIC---SDPWNRCC 60
                 |  ||:| |  |:     ||:  | :|||:   |       |  ||
Db         57 DSVPGLRKNMACY-----CRIPACLAGERRYGTCFYMGRVWAFCC 96


RESULT 15
Q9TTZ9
ID   Q9TTZ9      PRELIMINARY;      PRT;    96 AA.
AC   Q9TTZ9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Alpha-defensin 1A.
GN   MNP1A.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhao C., Nguyen T., Lehrer R.I.;
RT   "cDNA cloning of three alpha-defensins and three demidefensins from
RT   rhesus monkey bone marrow.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF184160; AAF07926.1; -.
DR   PIR; A59076; A59076.
DR   HSSP; P11479; 1DFN.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0003795; F:antimicrobial peptide activity; IEA.
DR   GO; GO:0006952; P:defense response; IEA.
DR   InterPro; IPR006081; Defensin_alpha.
DR   InterPro; IPR006080; Defensin_mammal.
DR   InterPro; IPR002366; Defensin_propep.
DR   Pfam; PF00323; defensins; 1.
DR   Pfam; PF00879; Defensin_propep; 1.
DR   SMART; SM00048; DEFSN; 1.
DR   PROSITE; PS00269; DEFENSIN; 1.
SQ   SEQUENCE   96 AA;  10516 MW;  A536B80CBFF575A2 CRC64;

  Query Match             17.3%;  Score 65.5;  DB 6;  Length 96;
  Best Local Similarity   35.6%;  Pred. No. 0.38;
  Matches   16;  Conservative    5;  Mismatches   15;  Indels    9;  Gaps    3;

Qy         20 DIPPGIR-NTVCFMQRGHCRLFMCRSGERKGDIC---SDPWNRCC 60
                 |  ||:| |  |:     ||:  | :|||:   |       |  ||
Db         57 DSVPGLRKNMACY-----CRIPACLAGERRYGTCFYLGRVWAFCC 96


Search completed: June 14, 2004, 16:40:33
Job time : 49 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 14, 2004, 16:28:58 ; Search time 56 Seconds
(without alignments)
343.093 Million cell updates/sec

Title: US-10-623-629-2
Perfect score: 379
Sequence: 1 MKVLLLFAVFFCLVQRNSGD.....GDICSDPWNRCCVSSSIKNR 68

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	379	100.0	68	5	ABB83977	Abb83977 Rat Binlb
2	286	75.5	80	4	AAB84567	Aab84567 Amino aci
3	276	72.8	80	4	AAB84568	Aab84568 Amino aci
4	260	68.6	45	5	ABB83978	Abb83978 Rat Binlb
5	227	59.9	64	4	AAB84579	Aab84579 Amino aci
6	217	57.3	62	4	AAB84588	Aab84588 Amino aci
7	217	57.3	64	4	AAB84580	Aab84580 Amino aci
8	217	57.3	109	4	AAB84577	Aab84577 Amino aci
9	217	57.3	133	4	AAB84565	Aab84565 Amino aci
10	207	54.6	62	4	AAB84589	Aab84589 Amino aci
11	207	54.6	109	4	AAB84578	Aab84578 Amino aci
12	207	54.6	133	4	AAB84566	Aab84566 Amino aci
13	197	52.0	35	6	ABR43520	Abr43520 Mouse bet
14	167	44.1	39	6	ABR43588	Abr43588 Human bet
15	165	43.5	35	6	ABR43519	Abr43519 Human bet
16	144	38.0	31	5	AAM49583	Aam49583 Human bet
17	76.5	20.2	123	4	AAB36670	Aab36670 Human sec
18	76.5	20.2	123	6	ADA56887	Ada56887 Human sec
19	76.5	20.2	123	6	ADA40741	Ada40741 Human sec
20	76.5	20.2	123	6	ABR47725	Abr47725 Human sec
21	76.5	20.2	124	2	AAY36298	Aay36298 Human sec
22	76.5	20.2	124	6	ADA11608	Ada11608 Human nov
23	75	19.8	64	5	AAU91052	Aau91052 Transplan
24	74	19.5	111	4	AAB47331	Aab47331 FCTR8. 8/
25	74	19.5	111	5	AAU83135	Aau83135 Novel sec
26	73	19.3	31	6	ABR43538	Abr43538 Mouse bet
27	72	19.0	50	4	AAB84561	Aab84561 Amino aci
28	72	19.0	64	5	AAU91051	Aau91051 Transplan
29	70.5	18.6	32	6	ABR43553	Abr43553 Mouse bet
30	69	18.2	50	4	AAB84562	Aab84562 Amino aci
31	69	18.2	548	4	AAB30572	Aab30572 A full le
32	68.5	18.1	87	4	AAM78915	Aam78915 Human pro
33	68.5	18.1	87	4	AAB60637	Aab60637 Human NAD
34	68.5	18.1	87	6	ABR58636	Abr58636 Human can
35	68.5	18.1	89	6	AAO22651	Aao22651 Maize bas
36	68.5	18.1	89	6	AAO22650	Aao22650 Maize bas
37	68.5	18.1	92	4	ABB03256	Abb03256 Human mus
38	68.5	18.1	92	6	ABU12550	Abu12550 Novel hum
39	67	17.7	37	6	ABR43597	Abr43597 Human bet
40	66	17.4	65	2	AAY07243	Aay07243 Beta-defe
41	66	17.4	67	2	AAY07244	Aay07244 Beta-defe
42	66	17.4	67	3	AAB10602	Aab10602 Human SAP
43	66	17.4	67	5	AAU09707	Aau09707 Human bet
44	66	17.4	67	5	AAU91016	Aau91016 Transplan
45	66	17.4	67	5	AAU91036	Aau91036 Transplan

ALIGNMENTS

RESULT 1
ABB83977
ID ABB83977 standard; protein; 68 AA.
XX
AC ABB83977;
XX
DT 09-DEC-2002 (first entry)
XX
DE Rat Binlb SEQ ID NO 2.
XX
KW Rat; Binlb; antibacterial; infection; urinogenital system;
KW sperm maturation.
XX
OS Rattus norvegicus.
XX
PN WO200268463-A1.
XX
PD 06-SEP-2002.
XX
PF 21-JAN-2002; 2002WO-CN000032.
XX
PR 22-JAN-2001; 2001CN-00105283.
XX
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
XX
PI Zhang Y, Chan H, Li P, He B, So S, Chung Y, Shang Q, Zhang Y;
XX
DR WPI; 2002-682810/73.
DR N-PSDB; ABV73546, ABV73553, ABV73554.
XX
PT Natural antibacterial Binlb proteins, and encoding polynucleotides,
PT associated with male reproduction especially sperm maturation, applicable
PT in treating disorders like infection of urinogenital system.
XX
PS Example 2; Fig 2A; 35pp; Chinese.
XX
CC The invention relates to an isolated or purified antibacterial Binlb
CC polypeptide. The peptide is for pharmaceutical compositions which are
CC applicable in treating disorders like infections of urinogenital system.
CC The polypeptide and its encoding polynucleotide are associated with male
CC reproduction especially sperm maturation. The present sequence is that of
CC the rat Binlb protein of the invention
XX
SQ Sequence 68 AA;

Query Match 100.0%; Score 379; DB 5; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.2e-36;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MKVLLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MKVLLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60

Qy         61 VSSSIKNR 68
              ||||||||
Db         61 VSSSIKNR 68
```

RESULT 2
AAB84567
ID AAB84567 standard; protein; 80 AA.
XX
AC AAB84567;
XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of a human EP2 peptide.
XX
KW Antimicrobial peptide; primate epididymis; EP2; microbial infection;
KW epithelial infection; epididymitis; urogenital tract infection;
KW sexually transmitted disease; condom.
XX
OS Homo sapiens.
XX
PN WO200149702-A1.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000432.
XX
PR 05-JAN-2000; 2000US-0174513P.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Froelich O, Young LG;
XX
DR WPI; 2001-418353/44.
DR N-PSDB; AAH28182.
XX
PT Antimicrobial peptides from primate epididymis, useful in the production
PT of condoms for preventing sexually transmitted diseases.
XX
PS Claim 6; Page 41; 81pp; English.
XX
CC The present sequence represents an antimicrobial peptide expressed in the
CC primate epididymis, designated EP2. The EP2 peptides are comprised of one
CC or more peptide modules (see AAB84583-89). The EP2 peptides are cationic
CC and interact with the membrane of invading pathogens to cause disruptive
CC changes in their permeability. Compositions comprising the EP2 peptides
CC and nucleic acids may be administered to treat microbial infections, to
CC supplement the endogenous production of EP2 peptides for resisting a
CC microbial infection. The EP2 peptides may be used to treat animals
CC (especially those suffering from epithelial infections (e.g.
CC epididymitis), urogenital tract infections and sexually transmitted
CC diseases) and humans and in agricultural and industrial applications.
CC Microorganisms susceptible to EP2 peptides include Neisseria gonorrhoeae,
CC Chlamydia trachomatis, Pseudomonas aeruginosa, Escherichia coli,
CC Staphylococcus aureus, Mycobacterium tuberculosis, Hemophilus influenzae,
CC Streptococcus pneumoniae, Brucella abortus, Brucella melitensis,
CC Aspergillus fumigatus, Candida albicans, Candida tropicalis,
CC Cytomegalovirus, ovine lentivirus (OvLV), filaria, schistosoma and/or
CC amebae. The EP2 peptides are especially suitable for use in the
CC production of male and female condoms
XX
SQ Sequence 80 AA;

```
  Query Match             75.5%;  Score 286;  DB 4;  Length 80;
  Best Local Similarity   76.6%;  Pred. No. 9.9e-26;
  Matches   49;  Conservative    6;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 MKVLLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              ||| |||| ||||| ||||:||||||:| ||:| |||| | |||:| ||||||||||||
Db          1 MKVFFLFAVLFCLVQTNSGDVPPGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCC 60

Qy         61 VSSS 64
              ||::
Db         61 VSNT 64
```

RESULT 3
AAB84568
ID AAB84568 standard; protein; 80 AA.
XX
AC AAB84568;
XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of a chimpanzee EP2 peptide.
XX
KW Antimicrobial peptide; primate epididymis; EP2; microbial infection;
KW epithelial infection; epididymitis; urogenital tract infection;
KW sexually transmitted disease; condom.
XX
OS Pan troglodytes.
XX
PN WO200149702-A1.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000432.
XX
PR 05-JAN-2000; 2000US-0174513P.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Froelich O, Young LG;
XX
DR WPI; 2001-418353/44.
DR N-PSDB; AAH28183.
XX
PT Antimicrobial peptides from primate epididymis, useful in the production
PT of condoms for preventing sexually transmitted diseases.
XX
PS Claim 6; Page 41; 81pp; English.
XX
CC The present sequence represents an antimicrobial peptide expressed in the
CC primate epididymis, designated EP2. The EP2 peptides are comprised of one
CC or more peptide modules (see AAB84583-89). The EP2 peptides are cationic
CC and interact with the membrane of invading pathogens to cause disruptive
CC changes in their permeability. Compositions comprising the EP2 peptides
CC and nucleic acids may be administered to treat microbial infections, to
CC supplement the endogenous production of EP2 peptides for resisting a
CC microbial infection. The EP2 peptides may be used to treat animals
CC (especially those suffering from epithelial infections (e.g.
CC epididymitis), urogenital tract infections and sexually transmitted
CC diseases) and humans and in agricultural and industrial applications.
CC Microorganisms susceptible to EP2 peptides include Neisseria gonorrhoeae,
CC Chlamydia trachomatis, Pseudomonas aeruginosa, Escherichia coli,
CC Staphylococcus aureus, Mycobacterium tuberculosis, Hemophilus influenzae,
CC Streptococcus pneumoniae, Brucella abortus, Brucella melitensis,
CC Aspergillus fumigatus, Candida albicans, Candida tropicalis,
CC Cytomegalovirus, ovine lentivirus (OvLV), filaria, schistosoma and/or
CC amebae. The EP2 peptides are especially suitable for use in the
CC production of male and female condoms
XX
SQ Sequence 80 AA;

```
  Query Match             72.8%;  Score 276;  DB 4;  Length 80;
  Best Local Similarity   75.0%;  Pred. No. 1.5e-24;
  Matches   48;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MKVLLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              ||| |||| ||||| ||||:||||||:| ||:| |||| | |||:| ||||||||||||
Db          1 MKVFFLFAVLFCLVQTNSGDVPLGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCC 60
```

```
Qy          61 VSSS 64
               ||::
Db          61 VSNT 64
```

RESULT 4
ABB83978
ID ABB83978 standard; protein; 45 AA.
XX
AC ABB83978;
XX
DT 09-DEC-2002 (first entry)
XX
DE Rat Binlb C-terminal region SEQ ID NO 3.
XX
KW Rat; Binlb; antibacterial; infection; urinogenital system;
KW sperm maturation.
XX
OS Rattus norvegicus.
XX
PN WO200268463-A1.
XX
PD 06-SEP-2002.
XX
PF 21-JAN-2002; 2002WO-CN000032.
XX
PR 22-JAN-2001; 2001CN-00105283.
XX
PA (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
XX
PI Zhang Y, Chan H, Li P, He B, So S, Chung Y, Shang Q, Zhang Y;
XX
DR WPI; 2002-682810/73.
XX
PT Natural antibacterial Binlb proteins, and encoding polynucleotides,
PT associated with male reproduction especially sperm maturation, applicable
PT in treating disorders like infection of urinogenital system.
XX
PS Example 2; Fig 2A; 35pp; Chinese.
XX
CC The invention relates to an isolated or purified antibacterial Binlb
CC polypeptide. The peptide is for pharmaceutical compositions which are
CC applicable in treating disorders like infections of urinogenital system.
CC The polypeptide and its encoding polynucleotide are associated with male
CC reproduction especially sperm maturation. The present sequence is that of
CC the C-terminal region of the rat Binlb protein of the invention
XX
SQ Sequence 45 AA;

  Query Match   68.6%; Score 260; DB 5; Length 45;
  Best Local Similarity   100.0%; Pred. No. 5.9e-23;
  Matches   45; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy          24 GIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSSIKNR 68
               |||||||||||||||||||||||||||||||||||||||||||||
Db           1 GIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSSIKNR 45
```

RESULT 5
AAB84579
ID AAB84579 standard; protein; 64 AA.
XX
AC AAB84579;
XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of a mature human EP2 peptide.
XX
KW Antimicrobial peptide; primate epididymis; EP2; microbial infection;
KW epithelial infection; epididymitis; urogenital tract infection;
KW sexually transmitted disease; condom.
XX
OS Homo sapiens.
XX
PN WO200149702-A1.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000432.
XX
PR 05-JAN-2000; 2000US-0174513P.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Froelich O, Young LG;
XX
DR WPI; 2001-418353/44.
XX
PT Antimicrobial peptides from primate epididymis, useful in the production
PT of condoms for preventing sexually transmitted diseases.
XX
PS Claim 3; Page 46; 81pp; English.
XX
CC AAB84571-82 represent mature antimicrobial peptides, expressed in the
CC primate epididymis, designated EP2. The EP2 peptides are comprised of one
CC or more peptide modules (see AAB84583-89). The EP2 peptides are cationic
CC and interact with the membrane of invading pathogens to cause disruptive
CC changes in their permeability. Compositions comprising the EP2 peptides
CC and nucleic acids may be administered to treat microbial infections, to
CC supplement the endogenous production of EP2 peptides for resisting a
CC microbial infection. The EP2 peptides may be used to treat animals
CC (especially those suffering from epithelial infections (e.g.
CC epididymitis), urogenital tract infections and sexually transmitted
CC diseases) and humans and in agricultural and industrial applications.
CC Microorganisms susceptible to EP2 peptides include Neisseria gonorrhoeae,
CC Chlamydia trachomatis, Pseudomonas aeruginosa, Escherichia coli,
CC Staphylococcus aureus, Mycobacterium tuberculosis, Hemophilus influenzae,
CC Streptococcus pneumoniae, Brucella abortus, Brucella melitensis,
CC Aspergillus fumigatus, Candida albicans, Candida tropicalis,
CC Cytomegalovirus, ovine lentivirus (OvLV), filaria, schistosoma and/or
CC amebae. The EP2 peptides are especially suitable for use in the
CC production of male and female condoms
XX
SQ Sequence 64 AA;

  Query Match   59.9%; Score 227; DB 4; Length 64;
  Best Local Similarity   77.1%; Pred. No. 6.1e-19;
  Matches   37; Conservative   6; Mismatches   5; Indels   0; Gaps   0;

```
Qy          17 NSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSS 64
               ||||:|||||||:| ||:| |||| | |||:| ||||||||||||::
Db           1 NSGDVPPGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCCVSNT 48
```

RESULT 6
AAB84588
ID AAB84588 standard; peptide; 62 AA.
XX
AC AAB84588;
XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of an EP2 peptide module.
XX
KW Antimicrobial peptide; primate epididymis; EP2; microbial infection;
KW epithelial infection; epididymitis; urogenital tract infection;
KW sexually transmitted disease; condom.
XX
OS Homo sapiens.
XX
PN WO200149702-A1.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000432.

XX
PR 05-JAN-2000; 2000US-0174513P.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Froelich O, Young LG;
XX
DR WPI; 2001-418353/44.
XX
PT Antimicrobial peptides from primate epididymis, useful in the production
PT of condoms for preventing sexually transmitted diseases.
XX
PS Claim 3; Page 49; 81pp; English.
XX
CC AAB84583-89 represent modules of antimicrobial peptides expressed in the
CC primate epididymis, designated EP2. The EP2 peptides are comprised of one
CC or more peptide modules (see AAB84583-89). The EP2 peptides are cationic
CC and interact with the membrane of invading pathogens to cause disruptive
CC changes in their permeability. Compositions comprising the EP2 peptides
CC and nucleic acids may be administered to treat microbial infections, to
CC supplement the endogenous production of EP2 peptides for resisting a
CC microbial infection. The EP2 peptides may be used to treat animals
CC (especially those suffering from epithelial infections (e.g.
CC epididymitis), urogenital tract infections and sexually transmitted
CC diseases) and humans and in agricultural and industrial applications.
CC Microorganisms susceptible to EP2 peptides include Neisseria gonorrhoeae,
CC Chlamydia trachomatis, Pseudomonas aeruginosa, Escherichia coli,
CC Staphylococcus aureus, Mycobacterium tuberculosis, Hemophilus influenzae,
CC Streptococcus pneumoniae, Brucella abortus, Brucella melitensis,
CC Aspergillus fumigatus, Candida albicans, Candida tropicalis,
CC Cytomegalovirus, ovine lentivirus (OvLV), filaria, schistosoma and/or
CC amebae. The EP2 peptides are especially suitable for use in the
CC production of male and female condoms
XX
SQ Sequence 62 AA;

Query Match 57.3%; Score 217; DB 4; Length 62;
Best Local Similarity 76.1%; Pred. No. 8.6e-18;
Matches 35; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

```
Qy         19 GDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSS 64
              ||:|||||||:| ||:| |||| | |||:| |||||||||||||::
Db          1 GDVPPGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCCVSNT 46
```

RESULT 7
AAB84580
ID AAB84580 standard; protein; 64 AA.
XX
AC AAB84580;
XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of a mature chimpanzee EP2 peptide.
XX
KW Antimicrobial peptide; primate epididymis; EP2; microbial infection;
KW epithelial infection; epididymitis; urogenital tract infection;
KW sexually transmitted disease; condom.
XX
OS Pan troglodytes.
XX
PN WO200149702-A1.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000432.
XX
PR 05-JAN-2000; 2000US-0174513P.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Froelich O, Young LG;
XX
DR WPI; 2001-418353/44.
XX
PT Antimicrobial peptides from primate epididymis, useful in the production
PT of condoms for preventing sexually transmitted diseases.
XX
PS Claim 3; Page 47; 81pp; English.
XX
CC AAB84571-82 represent mature antimicrobial peptides, expressed in the
CC primate epididymis, designated EP2. The EP2 peptides are comprised of one
CC or more peptide modules (see AAB84583-89). The EP2 peptides are cationic
CC and interact with the membrane of invading pathogens to cause disruptive
CC changes in their permeability. Compositions comprising the EP2 peptides
CC and nucleic acids may be administered to treat microbial infections, to
CC supplement the endogenous production of EP2 peptides for resisting a
CC microbial infection. The EP2 peptides may be used to treat animals
CC (especially those suffering from epithelial infections (e.g.
CC epididymitis), urogenital tract infections and sexually transmitted
CC diseases) and humans and in agricultural and industrial applications.
CC Microorganisms susceptible to EP2 peptides include Neisseria gonorrhoeae,
CC Chlamydia trachomatis, Pseudomonas aeruginosa, Escherichia coli,
CC Staphylococcus aureus, Mycobacterium tuberculosis, Hemophilus influenzae,
CC Streptococcus pneumoniae, Brucella abortus, Brucella melitensis,
CC Aspergillus fumigatus, Candida albicans, Candida tropicalis,
CC Cytomegalovirus, ovine lentivirus (OvLV), filaria, schistosoma and/or
CC amebae. The EP2 peptides are especially suitable for use in the
CC production of male and female condoms
XX
SQ Sequence 64 AA;

Query Match 57.3%; Score 217; DB 4; Length 64;
Best Local Similarity 75.0%; Pred. No. 8.9e-18;
Matches 36; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

```
Qy         17 NSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSS 64
              ||||:| |||||:| ||:| |||| | |||:| ||||||||||||::
Db          1 NSGDVPLGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCCVSNT 48
```

RESULT 8
AAB84577
ID AAB84577 standard; protein; 109 AA.
XX
AC AAB84577;
XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of a mature human EP2 peptide.
XX
KW Antimicrobial peptide; primate epididymis; EP2; microbial infection;
KW epithelial infection; epididymitis; urogenital tract infection;
KW sexually transmitted disease; condom.
XX
OS Homo sapiens.
XX
PN WO200149702-A1.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000432.
XX
PR 05-JAN-2000; 2000US-0174513P.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Froelich O, Young LG;
XX
DR WPI; 2001-418353/44.
XX
PT Antimicrobial peptides from primate epididymis, useful in the production
PT of condoms for preventing sexually transmitted diseases.
XX
PS Claim 3; Page 45; 81pp; English.
XX

CC AAB84571-82 represent mature antimicrobial peptides, expressed in the
CC primate epididymis, designated EP2. The EP2 peptides are comprised of one
CC or more peptide modules (see AAB84583-89). The EP2 peptides are cationic
CC and interact with the membrane of invading pathogens to cause disruptive
CC changes in their permeability. Compositions comprising the EP2 peptides
CC and nucleic acids may be administered to treat microbial infections, to
CC supplement the endogenous production of EP2 peptides for resisting a
CC microbial infection. The EP2 peptides may be used to treat animals
CC (especially those suffering from epithelial infections (e.g.
CC epididymitis), urogenital tract infections and sexually transmitted
CC diseases) and humans and in agricultural and industrial applications.
CC Microorganisms susceptible to EP2 peptides include Neisseria gonorrhoeae,
CC Chlamydia trachomatis, Pseudomonas aeruginosa, Escherichia coli,
CC Staphylococcus aureus, Mycobacterium tuberculosis, Hemophilus influenzae,
CC Streptococcus pneumoniae, Brucella abortus, Brucella melitensis,
CC Aspergillus fumigatus, Candida albicans, Candida tropicalis,
CC Cytomegalovirus, ovine lentivirus (OvLV), filaria, schistosoma and/or
CC amebae. The EP2 peptides are especially suitable for use in the
CC production of male and female condoms
XX
SQ Sequence 109 AA;

Query Match 57.3%; Score 217; DB 4; Length 109;
Best Local Similarity 76.1%; Pred. No. 1.5e-17;
Matches 35; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 19 GDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSS 64
||:|||||||:| ||:| |||| | |||:| ||||||||||||::
Db 48 GDVPPGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCCVSNT 93

RESULT 9
AAB84565
ID AAB84565 standard; protein; 133 AA.
XX
AC AAB84565;
XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of a human EP2 peptide.
XX
KW Antimicrobial peptide; primate epididymis; EP2; microbial infection;
KW epithelial infection; epididymitis; urogenital tract infection;
KW sexually transmitted disease; condom.
XX
OS Homo sapiens.
XX
PN WO200149702-A1.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000432.
XX
PR 05-JAN-2000; 2000US-0174513P.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Froelich O, Young LG;
XX
DR WPI; 2001-418353/44.
DR N-PSDB; AAH28180.
XX
PT Antimicrobial peptides from primate epididymis, useful in the production
PT of condoms for preventing sexually transmitted diseases.
XX
PS Claim 6; Page 39-40; 81pp; English.
XX
CC The present sequence represents an antimicrobial peptide expressed in the
CC primate epididymis, designated EP2. The EP2 peptides are comprised of one
CC or more peptide modules (see AAB84583-89). The EP2 peptides are cationic
CC and interact with the membrane of invading pathogens to cause disruptive
CC changes in their permeability. Compositions comprising the EP2 peptides
CC and nucleic acids may be administered to treat microbial infections, to
CC supplement the endogenous production of EP2 peptides for resisting a
CC microbial infection. The EP2 peptides may be used to treat animals
CC (especially those suffering from epithelial infections (e.g.
CC epididymitis), urogenital tract infections and sexually transmitted
CC diseases) and humans and in agricultural and industrial applications.
CC Microorganisms susceptible to EP2 peptides include Neisseria gonorrhoeae,
CC Chlamydia trachomatis, Pseudomonas aeruginosa, Escherichia coli,
CC Staphylococcus aureus, Mycobacterium tuberculosis, Hemophilus influenzae,
CC Streptococcus pneumoniae, Brucella abortus, Brucella melitensis,
CC Aspergillus fumigatus, Candida albicans, Candida tropicalis,
CC Cytomegalovirus, ovine lentivirus (OvLV), filaria, schistosoma and/or
CC amebae. The EP2 peptides are especially suitable for use in the
CC production of male and female condoms
XX
SQ Sequence 133 AA;

Query Match 57.3%; Score 217; DB 4; Length 133;
Best Local Similarity 76.1%; Pred. No. 1.9e-17;
Matches 35; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 19 GDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSS 64
||:|||||||:| ||:| |||| | |||:| ||||||||||||::
Db 72 GDVPPGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCCVSNT 117

RESULT 10
AAB84589
ID AAB84589 standard; peptide; 62 AA.
XX
AC AAB84589;
XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of an EP2 peptide module.
XX
KW Antimicrobial peptide; primate epididymis; EP2; microbial infection;
KW epithelial infection; epididymitis; urogenital tract infection;
KW sexually transmitted disease; condom.
XX
OS Pan troglodytes.
XX
PN WO200149702-A1.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000432.
XX
PR 05-JAN-2000; 2000US-0174513P.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Froelich O, Young LG;
XX
DR WPI; 2001-418353/44.
XX
PT Antimicrobial peptides from primate epididymis, useful in the production
PT of condoms for preventing sexually transmitted diseases.
XX
PS Claim 3; Page 50; 81pp; English.
XX
CC AAB84583-89 represent modules of antimicrobial peptides expressed in the
CC primate epididymis, designated EP2. The EP2 peptides are comprised of one
CC or more peptide modules (see AAB84583-89). The EP2 peptides are cationic
CC and interact with the membrane of invading pathogens to cause disruptive
CC changes in their permeability. Compositions comprising the EP2 peptides
CC and nucleic acids may be administered to treat microbial infections, to
CC supplement the endogenous production of EP2 peptides for resisting a
CC microbial infection. The EP2 peptides may be used to treat animals
CC (especially those suffering from epithelial infections (e.g.
CC epididymitis), urogenital tract infections and sexually transmitted
CC diseases) and humans and in agricultural and industrial applications.
CC Microorganisms susceptible to EP2 peptides include Neisseria gonorrhoeae,
CC Chlamydia trachomatis, Pseudomonas aeruginosa, Escherichia coli,

CC Staphylococcus aureus, Mycobacterium tuberculosis, Hemophilus influenzae,
CC Streptococcus pneumoniae, Brucella abortus, Brucella melitensis,
CC Aspergillus fumigatus, Candida albicans, Candida tropicalis,
CC Cytomegalovirus, ovine lentivirus (OvLV), filaria, schistosoma and/or
CC amebae. The EP2 peptides are especially suitable for use in the
CC production of male and female condoms
XX
SQ Sequence 62 AA;

Query Match 54.6%; Score 207; DB 4; Length 62;
Best Local Similarity 73.9%; Pred. No. 1.3e-16;
Matches 34; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 19 GDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSS 64
||:| |||||:| ||:| |||| | |||:| ||||||||||||||::
Db 1 GDVPLGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCCVSNT 46

RESULT 11
AAB84578
ID AAB84578 standard; protein; 109 AA.
XX
AC AAB84578;
XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of a mature chimpanzee EP2 peptide.
XX
KW Antimicrobial peptide; primate epididymis; EP2; microbial infection;
KW epithelial infection; epididymitis; urogenital tract infection;
KW sexually transmitted disease; condom.
XX
OS Pan troglodytes.
XX
PN WO200149702-A1.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000432.
XX
PR 05-JAN-2000; 2000US-0174513P.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Froelich O, Young LG;
XX
DR WPI; 2001-418353/44.
XX
PT Antimicrobial peptides from primate epididymis, useful in the production
PT of condoms for preventing sexually transmitted diseases.
XX
PS Claim 3; Page 46; 81pp; English.
XX
CC AAB84571-82 represent mature antimicrobial peptides, expressed in the
CC primate epididymis, designated EP2. The EP2 peptides are comprised of one
CC or more peptide modules (see AAB84583-89). The EP2 peptides are cationic
CC and interact with the membrane of invading pathogens to cause disruptive
CC changes in their permeability. Compositions comprising the EP2 peptides
CC and nucleic acids may be administered to treat microbial infections, to
CC supplement the endogenous production of EP2 peptides for resisting a
CC microbial infection. The EP2 peptides may be used to treat animals
CC (especially those suffering from epithelial infections (e.g.
CC epididymitis), urogenital tract infections and sexually transmitted
CC diseases) and humans and in agricultural and industrial applications.
CC Microorganisms susceptible to EP2 peptides include Neisseria gonorrhoeae,
CC Chlamydia trachomatis, Pseudomonas aeruginosa, Escherichia coli,
CC Staphylococcus aureus, Mycobacterium tuberculosis, Hemophilus influenzae,
CC Streptococcus pneumoniae, Brucella abortus, Brucella melitensis,
CC Aspergillus fumigatus, Candida albicans, Candida tropicalis,
CC Cytomegalovirus, ovine lentivirus (OvLV), filaria, schistosoma and/or
CC amebae. The EP2 peptides are especially suitable for use in the
CC production of male and female condoms
XX
SQ Sequence 109 AA;

Query Match 54.6%; Score 207; DB 4; Length 109;
Best Local Similarity 73.9%; Pred. No. 2.3e-16;
Matches 34; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 19 GDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSS 64
||:| |||||:| ||:| |||| | |||:| ||||||||||||||::
Db 48 GDVPLGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCCVSNT 93

RESULT 12
AAB84566
ID AAB84566 standard; protein; 133 AA.
XX
AC AAB84566;
XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of a chimpanzee EP2 peptide.
XX
KW Antimicrobial peptide; primate epididymis; EP2; microbial infection;
KW epithelial infection; epididymitis; urogenital tract infection;
KW sexually transmitted disease; condom.
XX
OS Pan troglodytes.
XX
PN WO200149702-A1.
XX
PD 12-JUL-2001.
XX
PF 05-JAN-2001; 2001WO-US000432.
XX
PR 05-JAN-2000; 2000US-0174513P.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Froelich O, Young LG;
XX
DR WPI; 2001-418353/44.
DR N-PSDB; AAH28181.
XX
PT Antimicrobial peptides from primate epididymis, useful in the production
PT of condoms for preventing sexually transmitted diseases.
XX
PS Claim 6; Page 40; 81pp; English.
XX
CC The present sequence represents an antimicrobial peptide expressed in the
CC primate epididymis, designated EP2. The EP2 peptides are comprised of one
CC or more peptide modules (see AAB84583-89). The EP2 peptides are cationic
CC and interact with the membrane of invading pathogens to cause disruptive
CC changes in their permeability. Compositions comprising the EP2 peptides
CC and nucleic acids may be administered to treat microbial infections, to
CC supplement the endogenous production of EP2 peptides for resisting a
CC microbial infection. The EP2 peptides may be used to treat animals
CC (especially those suffering from epithelial infections (e.g.
CC epididymitis), urogenital tract infections and sexually transmitted
CC diseases) and humans and in agricultural and industrial applications.
CC Microorganisms susceptible to EP2 peptides include Neisseria gonorrhoeae,
CC Chlamydia trachomatis, Pseudomonas aeruginosa, Escherichia coli,
CC Staphylococcus aureus, Mycobacterium tuberculosis, Hemophilus influenzae,
CC Streptococcus pneumoniae, Brucella abortus, Brucella melitensis,
CC Aspergillus fumigatus, Candida albicans, Candida tropicalis,
CC Cytomegalovirus, ovine lentivirus (OvLV), filaria, schistosoma and/or
CC amebae. The EP2 peptides are especially suitable for use in the
CC production of male and female condoms
XX
SQ Sequence 133 AA;

Query Match 54.6%; Score 207; DB 4; Length 133;
Best Local Similarity 73.9%; Pred. No. 2.8e-16;
Matches 34; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

```
Qy          19 GDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSS 64
               ||:| |||||:| ||:| |||| | |||:| ||||||||||||::
Db          72 GDVPLGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCCVSNT 117
```

RESULT 13
ABR43520
ID ABR43520 standard; peptide; 35 AA.
XX
AC ABR43520;
XX
DT 16-JUL-2003 (first entry)
XX
DE Mouse beta-defensin peptide EP2d/HE2b1 SEQ ID NO:25.
XX
KW Beta-defensin; antimicrobial; antibacterial; vaccine; gene therapy;
KW infection; antibiotic; chromosome 8.
XX
OS Mus musculus.
XX
PN WO2003024992-A2.
XX
PD 27-MAR-2003.
XX
PF 23-SEP-2002; 2002WO-US030106.
XX
PR 21-SEP-2001; 2001US-0323991P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Mccray PB, Schutte BC, Jia HP, Casavant TL, Welch MJ;
XX
DR WPI; 2003-354585/33.
XX
PT New antimicrobial peptides, beta-defensin, useful for preventing
PT microbial growth, for treating pulmonary infections, for reducing
PT resistance to antimicrobials and antibiotics, and for inhibiting
PT multidrug resistant bacteria.
XX
PS Claim 1; Page 78; 125pp; English.
XX
CC ABR43496 to ABR43577 represent beta-defensin antimicrobial peptides (I).
CC (I) have antibacterial activity and can be used in vaccines, and in gene
CC therapy. (I) can be used for preventing microbial growth, for treating
CC infections (e.g. pulmonary infections), for reducing resistance to
CC antimicrobials and antibiotics, and for inhibiting multidrug resistant
CC bacteria. The antimicrobial peptides may be included in food
CC preparations, pharmaceutical preparations, medicinal and pharmaceutical
CC products, cosmetic products, hygienic products, cleaning products and
CC cleaning agents, as well as to any material to which the peptides could
CC be sprayed on or adhered to where inhibition of microbial growth on such
CC material is desired. The antimicrobial peptides and nucleic acids
CC encoding them may be used in gene therapy. ABR43578 to ABR43610 represent
CC human beta-defensin peptides given in an example from the present
CC invention
XX
SQ Sequence 35 AA;

```
  Query Match             52.0%;  Score 197;  DB 6;  Length 35;
  Best Local Similarity   94.1%;  Pred. No. 1e-15;
  Matches   32;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          28 TVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCV 61
               ||| ||:|||||||||||||||||||||||||||
Db           1 TVCLMQQGHCRLFMCRSGERKGDICSDPWNRCCV 34
```

RESULT 14
ABR43588
ID ABR43588 standard; peptide; 39 AA.
XX
AC ABR43588;
XX
DT 16-JUL-2003 (first entry)
XX
DE Human beta-defensin peptide EP12d.
XX
KW Beta-defensin; antimicrobial; antibacterial; vaccine; gene therapy;
KW infection; antibiotic; chromosome 8.
XX
OS Homo sapiens.
XX
PN WO2003024992-A2.
XX
PD 27-MAR-2003.
XX
PF 23-SEP-2002; 2002WO-US030106.
XX
PR 21-SEP-2001; 2001US-0323991P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Mccray PB, Schutte BC, Jia HP, Casavant TL, Welch MJ;
XX
DR WPI; 2003-354585/33.
XX
PT New antimicrobial peptides, beta-defensin, useful for preventing
PT microbial growth, for treating pulmonary infections, for reducing
PT resistance to antimicrobials and antibiotics, and for inhibiting
PT multidrug resistant bacteria.
XX
PS Example 2; Fig 1; 125pp; English.
XX
CC ABR43496 to ABR43577 represent beta-defensin antimicrobial peptides (I).
CC (I) have antibacterial activity and can be used in vaccines, and in gene
CC therapy. (I) can be used for preventing microbial growth, for treating
CC infections (e.g. pulmonary infections), for reducing resistance to
CC antimicrobials and antibiotics, and for inhibiting multidrug resistant
CC bacteria. The antimicrobial peptides may be included in food
CC preparations, pharmaceutical preparations, medicinal and pharmaceutical
CC products, cosmetic products, hygienic products, cleaning products and
CC cleaning agents, as well as to any material to which the peptides could
CC be sprayed on or adhered to where inhibition of microbial growth on such
CC material is desired. The antimicrobial peptides and nucleic acids
CC encoding them may be used in gene therapy. ABR43578 to ABR43610 represent
CC human beta-defensin peptides given in an example from the present
CC invention
XX
SQ Sequence 39 AA;

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  Query Match             44.1%;  Score 167;  DB 6;  Length 39;
  Best Local Similarity   73.0%;  Pred. No. 3.7e-12;
  Matches   27;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          28 TVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSS 64
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Db           1 TICRMQQGICRLFFCHSGEKKRDICSDPWNRCCVSNT 37
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RESULT 15
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ID ABR43519 standard; peptide; 35 AA.
XX
AC ABR43519;
XX
DT 16-JUL-2003 (first entry)
XX
DE Human beta-defensin peptide EP2d/HE2b1 SEQ ID NO:24.
XX
KW Beta-defensin; antimicrobial; antibacterial; vaccine; gene therapy;
KW infection; antibiotic; chromosome 8p23-p22.
XX
OS Homo sapiens.
XX
PN WO2003024992-A2.
XX

PD 27-MAR-2003.
XX
PF 23-SEP-2002; 2002WO-US030106.
XX
PR 21-SEP-2001; 2001US-0323991P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Mccray PB, Schutte BC, Jia HP, Casavant TL, Welch MJ;
XX
DR WPI; 2003-354585/33.
XX
PT New antimicrobial peptides, beta-defensin, useful for preventing
PT microbial growth, for treating pulmonary infections, for reducing
PT resistance to antimicrobials and antibiotics, and for inhibiting
PT multidrug resistant bacteria.
XX
PS Claim 1; Page 78; 125pp; English.
XX
CC ABR43496 to ABR43577 represent beta-defensin antimicrobial peptides (I).
CC (I) have antibacterial activity and can be used in vaccines, and in gene
CC therapy. (I) can be used for preventing microbial growth, for treating
CC infections (e.g. pulmonary infections), for reducing resistance to
CC antimicrobials and antibiotics, and for inhibiting multidrug resistant
CC bacteria. The antimicrobial peptides may be included in food
CC preparations, pharmaceutical preparations, medicinal and pharmaceutical
CC products, cosmetic products, hygienic products, cleaning products and
CC cleaning agents, as well as to any material to which the peptides could
CC be sprayed on or adhered to where inhibition of microbial growth on such
CC material is desired. The antimicrobial peptides and nucleic acids
CC encoding them may be used in gene therapy. ABR43578 to ABR43610 represent
CC human beta-defensin peptides given in an example from the present
CC invention
XX
SQ Sequence 35 AA;

Query Match 43.5%; Score 165; DB 6; Length 35;
Best Local Similarity 77.1%; Pred. No. 5.6e-12;
Matches 27; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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              |:| ||:| |||| | |||:| ||||||||||||
Db          1 TICRMQQGICRLFFCHSGEKKRDICSDPWNRCCVS 35
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Search completed: June 14, 2004, 16:39:06
Job time : 57 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 14, 2004, 16:38:04 ; Search time 25 Seconds
(without alignments)
140.423 Million cell updates/sec

Title: US-10-623-629-2
Perfect score: 379
Sequence: 1 MKVLLLFAVFFCLVQRNSGD.....GDICSDPWNRCCVSSSIKNR 68

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	66	17.4	65	4	US-09-636-399A-2	Sequence 2, Appli
2	66	17.4	67	4	US-09-636-399A-10	Sequence 10, Appl
3	65.5	17.3	1665	4	US-09-858-664A-2	Sequence 2, Appli
4	65.5	17.3	1665	4	US-10-274-978-2	Sequence 2, Appli
5	63.5	16.8	40	1	US-08-033-873-9	Sequence 9, Appli
6	63.5	16.8	40	2	US-08-356-832-9	Sequence 9, Appli
7	63.5	16.8	40	3	US-08-988-705-9	Sequence 9, Appli
8	63	16.6	3635	4	US-09-845-583A-2	Sequence 2, Appli
9	62.5	16.5	40	1	US-08-033-873-7	Sequence 7, Appli
10	62.5	16.5	40	2	US-08-356-832-7	Sequence 7, Appli
11	62.5	16.5	40	3	US-08-988-705-7	Sequence 7, Appli
12	62.5	16.5	42	1	US-08-033-873-3	Sequence 3, Appli
13	62.5	16.5	42	2	US-08-356-832-3	Sequence 3, Appli
14	62.5	16.5	42	3	US-08-988-705-3	Sequence 3, Appli
15	62	16.4	64	1	US-08-248-016-4	Sequence 4, Appli
16	62	16.4	64	1	US-08-451-501-4	Sequence 4, Appli
17	62	16.4	64	2	US-08-713-455A-5	Sequence 5, Appli
18	62	16.4	64	4	US-09-228-302-8	Sequence 8, Appli
19	62	16.4	64	5	PCT-US95-06761-4	Sequence 4, Appli
20	62	16.4	65	1	US-08-248-016-12	Sequence 12, Appl
21	62	16.4	65	1	US-08-451-501-12	Sequence 12, Appl
22	62	16.4	65	5	PCT-US95-06761-12	Sequence 12, Appl
23	62	16.4	94	4	US-09-486-580A-3	Sequence 3, Appli
24	60	15.8	64	4	US-09-351-657A-4	Sequence 4, Appli
25	60	15.8	64	4	US-09-351-657A-8	Sequence 8, Appli
26	59.5	15.7	408	4	US-09-252-991A-30312	Sequence 30312, A
27	57.5	15.2	38	1	US-08-033-873-8	Sequence 8, Appli
28	57.5	15.2	38	2	US-08-356-832-8	Sequence 8, Appli
29	57.5	15.2	38	3	US-08-988-705-8	Sequence 8, Appli
30	57.5	15.2	41	1	US-08-033-873-4	Sequence 4, Appli
31	57.5	15.2	41	2	US-08-356-832-4	Sequence 4, Appli
32	57.5	15.2	41	3	US-08-988-705-4	Sequence 4, Appli
33	57.5	15.2	1010	3	US-08-882-046-7	Sequence 7, Appli
34	57.5	15.2	1036	4	US-09-068-740A-6	Sequence 6, Appli
35	57.5	15.2	1187	4	US-09-068-740A-7	Sequence 7, Appli
36	57.5	15.2	1208	4	US-09-199-865-1	Sequence 1, Appli
37	57.5	15.2	1218	2	US-08-400-159-6	Sequence 6, Appli
38	57.5	15.2	1218	3	US-08-611-729A-6	Sequence 6, Appli
39	57.5	15.2	1218	3	US-08-882-046-2	Sequence 2, Appli
40	57.5	15.2	1218	3	US-09-214-278-7	Sequence 7, Appli
41	57.5	15.2	1218	4	US-09-068-740A-11	Sequence 11, Appl
42	57.5	15.2	1218	4	US-09-855-722-7	Sequence 7, Appli
43	57	15.0	716	4	US-09-252-991A-30683	Sequence 30683, A
44	57	15.0	2556	1	US-08-083-590A-20	Sequence 20, Appl
45	57	15.0	2556	3	US-08-532-384-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-636-399A-2
; Sequence 2, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS
; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-636-399A-2

Query Match 17.4%; Score 66; DB 4; Length 65;
Best Local Similarity 31.7%; Pred. No. 0.39;
Matches 19; Conservative 8; Mismatches 27; Indels 6; Gaps 2;

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Db          6 LLFALLFLFLVPVPGH--GGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCC 63
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RESULT 2
US-09-636-399A-10
; Sequence 10, Application US/09636399A
; Patent No. 6576755
; GENERAL INFORMATION:
; APPLICANT: Adler, David A.
; APPLICANT: Holloway, James L.
; APPLICANT: Baindur, Nand
; APPLICANT: Beigel-Orme, Stephanie
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: NOVEL BETA-DEFENSINS

; FILE REFERENCE: 97-44C2
; CURRENT APPLICATION NUMBER: US/09/636,399A
; CURRENT FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/058,335
; PRIOR FILING DATE: 1997-10-09
; PRIOR APPLICATION NUMBER: 60/064,294
; PRIOR FILING DATE: 1997-11-05
; PRIOR APPLICATION NUMBER: 09/150,786
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/636,399
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
;   LENGTH: 67
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-636-399A-10

  Query Match   17.4%; Score 66; DB 4; Length 67;
  Best Local Similarity   31.7%; Pred. No. 0.4;
  Matches   19; Conservative   8; Mismatches   27; Indels   6; Gaps   2;

Qy   5 LLFAVFFCLVQRNSGDIPPGIRNTV----CFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
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RESULT 3
US-09-858-664A-2
; Sequence 2, Application US/09858664A
; Patent No. 6482624
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000927-CIP
; CURRENT APPLICATION NUMBER: US/09/858,664A
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-11
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 1665
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-858-664A-2

  Query Match   17.3%; Score 65.5; DB 4; Length 1665;
  Best Local Similarity   30.0%; Pred. No. 15;
  Matches   15; Conservative   9; Mismatches   19; Indels   7; Gaps   1;

Qy   24 GIRNTVCFMQRGHCRLFMCRSGERKG-------DICSDPWNRCCVSSSIK 66
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Db   1568 GARDLQRGLRKGLVRLSRCYAGLSGGAVAFLRSTLCAQPWGRPCASSCLQ 1617

RESULT 4
US-10-274-978-2
; Sequence 2, Application US/10274978
; Patent No. 6670164
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui, et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL000927-CIP-DIV
; CURRENT APPLICATION NUMBER: US/10/274,978
; CURRENT FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 09/858,664
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 09/711,134
; PRIOR FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 1665
;   TYPE: PRT
;   ORGANISM: Human
US-10-274-978-2

  Query Match   17.3%; Score 65.5; DB 4; Length 1665;
  Best Local Similarity   30.0%; Pred. No. 15;
  Matches   15; Conservative   9; Mismatches   19; Indels   7; Gaps   1;

Qy   24 GIRNTVCFMQRGHCRLFMCRSGERKG-------DICSDPWNRCCVSSSIK 66
              | |:   :::| || | :| | :|: || | | || ::
Db   1568 GARDLQRGLRKGLVRLSRCYAGLSGGAVAFLRSTLCAQPWGRPCASSCLQ 1617

RESULT 5
US-08-033-873-9
; Sequence 9, Application US/08033873
; Patent No. 5459235
; GENERAL INFORMATION:
;   APPLICANT: SELSTED, MICHAEL E.
;   APPLICANT: CULLOR, JAMES S.
;   TITLE OF INVENTION: NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
;   TITLE OF INVENTION: NEUTROPHILS
;   NUMBER OF SEQUENCES: 22
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: CAMPBELL AND FLORES
;   STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
;   CITY: SAN DIEGO
;   STATE: CALIFORNIA
;   COUNTRY: USA
;   ZIP: 92122
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/033,873
;   FILING DATE: 19930319
;   CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;   NAME: CAMPBELL, CATHRYN A.
;   REGISTRATION NUMBER: 31,815
;   REFERENCE/DOCKET NUMBER: P-UC 9552
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (619) 535-9001
;   TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 40 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-033-873-9

  Query Match   16.8%; Score 63.5; DB 1; Length 40;
  Best Local Similarity   36.8%; Pred. No. 0.47;
  Matches   14; Conservative   4; Mismatches   19; Indels   1; Gaps   1;

Qy   24 GIRNTV-CFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
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Db   2 GVRNFVTCRINRGFCVPIRCPGHRRQIGTCLGPQIKCC 39

RESULT 6
US-08-356-832-9
; Sequence 9, Application US/08356832
; Patent No. 5821224

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;  GENERAL INFORMATION:
;    APPLICANT:  SELSTED, MICHAEL E.
;    APPLICANT:  CULLOR, JAMES S.
;    TITLE OF INVENTION:  NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
;    TITLE OF INVENTION:  NEUTROPHILS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CAMPBELL AND FLORES
;      STREET:  4370 LA JOLLA VILLAGE DRIVE, SUITE 700
;      CITY:  SAN DIEGO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/356,832
;      FILING DATE:  12-DEC-1994
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/033,873
;      FILING DATE:  19-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CAMPBELL, CATHRYN A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 9552
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-356-832-9

  Query Match             16.8%;  Score 63.5;  DB 2;  Length 40;
  Best Local Similarity   36.8%;  Pred. No. 0.47;
  Matches   14;  Conservative    4;  Mismatches   19;  Indels    1;  Gaps    1;

Qy         24 GIRNTV-CFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
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Db          2 GVRNFVTCRINRGFCVPIRCPGHRRQIGTCLGPQIKCC 39


RESULT 7
US-08-988-705-9
; Sequence 9, Application US/08988705
; Patent No. 6211148
;  GENERAL INFORMATION:
;    APPLICANT:  Selsted, Michael E.
;    APPLICANT:  Cullor, James S.
;    TITLE OF INVENTION:  NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
;    TITLE OF INVENTION:  NEUTROPHILS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CAMPBELL & FLORES, LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/988,705
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/033,873
;      FILING DATE:  19-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/356,832
;      FILING DATE:  13-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 2918
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)535-9001
;      TELEFAX:  (619)535-8949
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-988-705-9

  Query Match             16.8%;  Score 63.5;  DB 3;  Length 40;
  Best Local Similarity   36.8%;  Pred. No. 0.47;
  Matches   14;  Conservative    4;  Mismatches   19;  Indels    1;  Gaps    1;

Qy         24 GIRNTV-CFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
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Db          2 GVRNFVTCRINRGFCVPIRCPGHRRQIGTCLGPQIKCC 39


RESULT 8
US-09-845-583A-2
; Sequence 2, Application US/09845583A
; Patent No. 6635616
; GENERAL INFORMATION:
;  APPLICANT: Burgeson, Robert
;  APPLICANT:  Brunken, William Joseph
;  APPLICANT:  Champliaud, Marie-France
;  APPLICANT:  Hunter, Dale
;  TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
;  FILE REFERENCE: 10287-056001
;  CURRENT APPLICATION NUMBER: US/09/845,583A
;  CURRENT FILING DATE:  2001-04-30
;  PRIOR APPLICATION NUMBER: US 60/200,863
;  PRIOR FILING DATE: 2000-05-01
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 3635
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-845-583A-2

  Query Match             16.6%;  Score 63;  DB 4;  Length 3635;
  Best Local Similarity   43.3%;  Pred. No. 69;
  Matches   13;  Conservative    6;  Mismatches    7;  Indels    4;  Gaps    2;

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Db        469 PGVANSLCDPESGQC---MCRTG-FEGDRC 494


RESULT 9
US-08-033-873-7
; Sequence 7, Application US/08033873
; Patent No. 5459235
;  GENERAL INFORMATION:
;    APPLICANT:  SELSTED, MICHAEL E.
;    APPLICANT:  CULLOR, JAMES S.
;    TITLE OF INVENTION:  NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
;    TITLE OF INVENTION:  NEUTROPHILS
```

```
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CAMPBELL AND FLORES
;      STREET:  4370 LA JOLLA VILLAGE DRIVE, SUITE 700
;      CITY:  SAN DIEGO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/033,873
;      FILING DATE:  19930319
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CAMPBELL, CATHRYN A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 9552
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-033-873-7

  Query Match             16.5%;  Score 62.5;  DB 1;  Length 40;
  Best Local Similarity   36.8%;  Pred. No. 0.62;
  Matches   14;  Conservative    4;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          24 GIRNTV-CFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
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Db           2 GVRNFVTCRINRGFCVPIRCPGHRRQIGTCLGPRIKCC 39


RESULT 10
US-08-356-832-7
; Sequence 7, Application US/08356832
; Patent No. 5821224
;  GENERAL INFORMATION:
;    APPLICANT:  SELSTED, MICHAEL E.
;    APPLICANT:  CULLOR, JAMES S.
;    TITLE OF INVENTION:  NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
;    TITLE OF INVENTION:  NEUTROPHILS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CAMPBELL AND FLORES
;      STREET:  4370 LA JOLLA VILLAGE DRIVE, SUITE 700
;      CITY:  SAN DIEGO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/356,832
;      FILING DATE:  12-DEC-1994
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/033,873
;      FILING DATE:  19-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CAMPBELL, CATHRYN A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 9552
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-356-832-7

  Query Match             16.5%;  Score 62.5;  DB 2;  Length 40;
  Best Local Similarity   36.8%;  Pred. No. 0.62;
  Matches   14;  Conservative    4;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          24 GIRNTV-CFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
               |:|| | | : || |    |    |:   | . |  :||
Db           2 GVRNFVTCRINRGFCVPIRCPGHRRQIGTCLGPRIKCC 39


RESULT 11
US-08-988-705-7
; Sequence 7, Application US/08988705
; Patent No. 6211148
;  GENERAL INFORMATION:
;    APPLICANT:  Selsted, Michael E.
;    APPLICANT:  Cullor, James S.
;    TITLE OF INVENTION:  NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
;    TITLE OF INVENTION:  NEUTROPHILS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CAMPBELL & FLORES, LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/988,705
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/033,873
;      FILING DATE:  19-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/356,832
;      FILING DATE:  13-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 2918
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)535-9001
;      TELEFAX:  (619)535-8949
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-988-705-7

  Query Match             16.5%;  Score 62.5;  DB 3;  Length 40;
  Best Local Similarity   36.8%;  Pred. No. 0.62;
  Matches   14;  Conservative    4;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          24 GIRNTV-CFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
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Db          2 GVRNFVTCRINRGFCVPIRCPGHRRQIGTCLGPRIKCC 39


RESULT 12
US-08-033-873-3
; Sequence 3, Application US/08033873
; Patent No. 5459235
;  GENERAL INFORMATION:
;    APPLICANT:  SELSTED, MICHAEL E.
;    APPLICANT:  CULLOR, JAMES S.
;    TITLE OF INVENTION:  NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
;    TITLE OF INVENTION:  NEUTROPHILS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CAMPBELL AND FLORES
;      STREET:  4370 LA JOLLA VILLAGE DRIVE, SUITE 700
;      CITY:  SAN DIEGO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/033,873
;      FILING DATE:  19930319
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CAMPBELL, CATHRYN A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 9552
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  42 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-033-873-3

  Query Match             16.5%;  Score 62.5;  DB 1;  Length 42;
  Best Local Similarity   37.5%;  Pred. No. 0.65;
  Matches   15;  Conservative    4;  Mismatches   20;  Indels    1;  Gaps    1;

Qy         24 GIRNTV-CFMQRGHCRLFMCRSGERKGDICSDPWNRCCVS 62
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Db          2 GVRNHVTCRINRGFCVPIRCPGRTRQIGTCFGPRIKCCRS 41


RESULT 13
US-08-356-832-3
; Sequence 3, Application US/08356832
; Patent No. 5821224
;  GENERAL INFORMATION:
;    APPLICANT:  SELSTED, MICHAEL E.
;    APPLICANT:  CULLOR, JAMES S.
;    TITLE OF INVENTION:  NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
;    TITLE OF INVENTION:  NEUTROPHILS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CAMPBELL AND FLORES
;      STREET:  4370 LA JOLLA VILLAGE DRIVE, SUITE 700
;      CITY:  SAN DIEGO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/356,832
;      FILING DATE:  12-DEC-1994
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/033,873
;      FILING DATE:  19-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CAMPBELL, CATHRYN A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 9552
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  42 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-356-832-3

  Query Match             16.5%;  Score 62.5;  DB 2;  Length 42;
  Best Local Similarity   37.5%;  Pred. No. 0.65;
  Matches   15;  Conservative    4;  Mismatches   20;  Indels    1;  Gaps    1;

Qy         24 GIRNTV-CFMQRGHCRLFMCRSGERKGDICSDPWNRCCVS 62
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Db          2 GVRNHVTCRINRGFCVPIRCPGRTRQIGTCFGPRIKCCRS 41


RESULT 14
US-08-988-705-3
; Sequence 3, Application US/08988705
; Patent No. 6211148
;  GENERAL INFORMATION:
;    APPLICANT:  Selsted, Michael E.
;    APPLICANT:  Cullor, James S.
;    TITLE OF INVENTION:  NOVEL ANTIMICROBIAL PEPTIDES FROM BOVINE
;    TITLE OF INVENTION:  NEUTROPHILS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CAMPBELL & FLORES, LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  United States
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/988,705
;      FILING DATE:
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/033,873
;      FILING DATE:  19-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/356,832
;      FILING DATE:  13-DEC-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UC 2918
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619)535-9001
;      TELEFAX:  (619)535-8949
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;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  42 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-988-705-3

  Query Match             16.5%;  Score 62.5;  DB 3;  Length 42;
  Best Local Similarity   37.5%;  Pred. No. 0.65;
  Matches   15;  Conservative    4;  Mismatches   20;  Indels    1;  Gaps    1;

Qy         24 GIRNTV-CFMQRGHCRLFMCRSGERKGDICSDPWNRCCVS 62
              |:|| | | : || |    |    |:   | |  :|| |
Db          2 GVRNHVTCRINRGFCVPIRCPGRTRQIGTCFGPRIKCCRS 41


RESULT 15
US-08-248-016-4
; Sequence 4, Application US/08248016
; Patent No. 5550109
;  GENERAL INFORMATION:
;    APPLICANT:  Schonwetter, Barry S.
;    APPLICANT:  Zasloff, Michael A.
;    TITLE OF INVENTION:  Inducible Defensin Peptide From
;    TITLE OF INVENTION:  Mammalian Epithelia
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washgington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/248,016
;      FILING DATE:  24-MAY-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ogden, Stasia L.
;      REGISTRATION NUMBER:  36,228
;      REFERENCE/DOCKET NUMBER:  05387.0017-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  64 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-248-016-4

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  Best Local Similarity   29.8%;  Pred. No. 1.2;
  Matches   17;  Conservative    8;  Mismatches   30;  Indels    2;  Gaps    2;

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GenCore version 5.1.6

OM protein - protein search, using sw model

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(without alignments)
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Title: US-10-623-629-2
Perfect score: 379
Sequence: 1 MKVLLLFAVFFCLVQRNSGD.....GDICSDPWNRCCVSSSIKNR 68

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1158786 seqs, 281726120 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	379	100.0	68	12	US-10-623-629-2	Sequence 2, Appli
2	286	75.5	80	12	US-10-381-752-9	Sequence 9, Appli
3	276	72.8	80	12	US-10-381-752-10	Sequence 10, Appl
4	260	68.6	45	12	US-10-623-629-3	Sequence 3, Appli
5	227	59.9	64	12	US-10-381-752-21	Sequence 21, Appl
6	217	57.3	62	12	US-10-381-752-30	Sequence 30, Appl
7	217	57.3	64	12	US-10-381-752-22	Sequence 22, Appl
8	217	57.3	109	12	US-10-381-752-19	Sequence 19, Appl
9	217	57.3	133	12	US-10-381-752-7	Sequence 7, Appli
10	207	54.6	62	12	US-10-381-752-31	Sequence 31, Appl
11	207	54.6	109	12	US-10-381-752-20	Sequence 20, Appl
12	207	54.6	133	12	US-10-381-752-8	Sequence 8, Appli
13	197	52.0	35	14	US-10-252-734-25	Sequence 25, Appl
14	165	43.5	35	14	US-10-252-734-24	Sequence 24, Appl
15	76.5	20.2	124	12	US-10-372-876-136	Sequence 136, App
16	76.5	20.2	124	14	US-10-097-065-136	Sequence 136, App
17	75	19.8	64	9	US-09-917-340-88	Sequence 88, Appl
18	74	19.5	111	9	US-09-893-737-122	Sequence 122, App
19	74	19.5	111	9	US-09-746-491-16	Sequence 16, Appl
20	73	19.3	31	14	US-10-252-734-43	Sequence 43, Appl
21	72	19.0	50	12	US-10-381-752-3	Sequence 3, Appli
22	72	19.0	64	9	US-09-917-340-87	Sequence 87, Appl
23	70.5	18.6	32	14	US-10-252-734-58	Sequence 58, Appl
24	69	18.2	50	12	US-10-381-752-4	Sequence 4, Appli
25	69	18.2	548	14	US-10-307-019-9	Sequence 9, Appli
26	68.5	18.1	89	14	US-10-205-072-10	Sequence 10, Appl
27	68.5	18.1	89	14	US-10-205-072-12	Sequence 12, Appl
28	68.5	18.1	92	9	US-09-764-877-1203	Sequence 1203, Ap
29	68.5	18.1	92	15	US-10-242-515-1203	Sequence 1203, Ap
30	66	17.4	65	14	US-10-091-166B-2	Sequence 2, Appli
31	66	17.4	65	14	US-10-272-121-2	Sequence 2, Appli
32	66	17.4	65	14	US-10-409-366-2	Sequence 2, Appli
33	66	17.4	65	14	US-10-409-532-2	Sequence 2, Appli
34	66	17.4	67	9	US-09-917-340-52	Sequence 52, Appl
35	66	17.4	67	9	US-09-917-340-72	Sequence 72, Appl
36	66	17.4	67	9	US-09-872-852-2	Sequence 2, Appli
37	66	17.4	67	14	US-10-091-166B-10	Sequence 10, Appl
38	66	17.4	67	14	US-10-272-121-10	Sequence 10, Appl
39	66	17.4	67	14	US-10-409-366-10	Sequence 10, Appl
40	66	17.4	67	14	US-10-409-532-10	Sequence 10, Appl
41	65.5	17.3	96	9	US-09-917-340-90	Sequence 90, Appl
42	65.5	17.3	390	12	US-10-425-114-37530	Sequence 37530, A
43	65.5	17.3	871	14	US-10-307-019-7	Sequence 7, Appli
44	65.5	17.3	871	16	US-10-311-034-20	Sequence 20, Appl
45	65.5	17.3	1351	14	US-10-307-019-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-10-623-629-2
; Sequence 2, Application US/10623629
; Publication No. US20040058371A1
; GENERAL INFORMATION:
; APPLICANT: SHANGHAI INSTITUTE OF BIOCHEMISTRY, CHINESE ACADEMY OF SCIENCES
; TITLE OF INVENTION: A NOVEL NATURAL ANTIBACTERIAL PEPTIDE, THE NUCLEOTIDE SEQUENCE EN
; TITLE OF INVENTION: IT AND THE
; TITLE OF INVENTION: USE THEREOF
; FILE REFERENCE: 010207 PCWO
; CURRENT APPLICATION NUMBER: US/10/623,629
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: CN 01105283.X
; PRIOR FILING DATE: 2001-01-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-629-2

Query Match 100.0%; Score 379; DB 12; Length 68;
Best Local Similarity 100.0%; Pred. No. 5.8e-38;
Matches 68; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 VSSSIKNR 68
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Db         61 VSSSIKNR 68
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RESULT 2
US-10-381-752-9
; Sequence 9, Application US/10381752

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; Publication No. US20040072777A1
; GENERAL INFORMATION:
;  APPLICANT: Froehlich, Otto
;  APPLICANT:  Young, Leona G.
;  TITLE OF INVENTION: Epididymal Antimicrobial Peptides
;  FILE REFERENCE: 05501-0132US  43150-251426
;  CURRENT APPLICATION NUMBER: US/10/381,752
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: PCT/US01/00432
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/174,513
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 80
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-381-752-9

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Qy          1 MKVLLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              |||  |||| ||||| ||||:|||||||:| ||:| |||| | |||:| ||||||||||
Db          1 MKVFFLFAVLFCLVQTNSGDVPPGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCC 60

Qy         61 VSSS 64
              ||::
Db         61 VSNT 64


RESULT 3
US-10-381-752-10
; Sequence 10, Application US/10381752
; Publication No. US20040072777A1
; GENERAL INFORMATION:
;  APPLICANT: Froehlich, Otto
;  APPLICANT:  Young, Leona G.
;  TITLE OF INVENTION: Epididymal Antimicrobial Peptides
;  FILE REFERENCE: 05501-0132US  43150-251426
;  CURRENT APPLICATION NUMBER: US/10/381,752
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: PCT/US01/00432
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/174,513
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 80
;   TYPE: PRT
;   ORGANISM: Pan troglodytes
US-10-381-752-10

  Query Match             72.8%;  Score 276;  DB 12;  Length 80;
  Best Local Similarity   75.0%;  Pred. No. 1.6e-25;
  Matches   48;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 MKVLLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              |||  |||| ||||| ||||:| |||||:| ||:| |||| | |||:| ||||||||||
Db          1 MKVFFLFAVLFCLVQTNSGDVPLGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCC 60

Qy         61 VSSS 64
              ||::
Db         61 VSNT 64


RESULT 4
US-10-623-629-3
; Sequence 3, Application US/10623629
; Publication No. US20040058371A1
; GENERAL INFORMATION:
;  APPLICANT: SHANGHAI INSTITUTE OF BIOCHEMISTRY, CHINESE ACADEMY OF SCIENCES
;  TITLE OF INVENTION: A NOVEL NATURAL ANTIBACTERIAL PEPTIDE, THE NUCLEOTIDE SEQUENCE EN
;  TITLE OF INVENTION:  IT AND THE
;  TITLE OF INVENTION:  USE THEREOF
;  FILE REFERENCE: 010207 PCWO
;  CURRENT APPLICATION NUMBER: US/10/623,629
;  CURRENT FILING DATE:  2003-07-21
;  PRIOR APPLICATION NUMBER: CN 01105283.X
;  PRIOR FILING DATE: 2001-01-22
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 45
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-623-629-3

  Query Match             68.6%;  Score 260;  DB 12;  Length 45;
  Best Local Similarity   100.0%;  Pred. No. 7.4e-24;
  Matches   45;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         24 GIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSSIKNR 68
              |||||||||||||||||||||||||||||||||||||||||||||
Db          1 GIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSSIKNR 45


RESULT 5
US-10-381-752-21
; Sequence 21, Application US/10381752
; Publication No. US20040072777A1
; GENERAL INFORMATION:
;  APPLICANT: Froehlich, Otto
;  APPLICANT:  Young, Leona G.
;  TITLE OF INVENTION: Epididymal Antimicrobial Peptides
;  FILE REFERENCE: 05501-0132US  43150-251426
;  CURRENT APPLICATION NUMBER: US/10/381,752
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: PCT/US01/00432
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/174,513
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
;   LENGTH: 64
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-381-752-21

  Query Match             59.9%;  Score 227;  DB 12;  Length 64;
  Best Local Similarity   77.1%;  Pred. No. 9.7e-20;
  Matches   37;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         17 NSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSS 64
              ||||:|||||||:| ||:| |||| | |||:| ||||||||||||::
Db          1 NSGDVPPGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCCVSNT 48


RESULT 6
US-10-381-752-30
; Sequence 30, Application US/10381752
; Publication No. US20040072777A1
; GENERAL INFORMATION:
;  APPLICANT: Froehlich, Otto
;  APPLICANT:  Young, Leona G.
;  TITLE OF INVENTION: Epididymal Antimicrobial Peptides
;  FILE REFERENCE: 05501-0132US  43150-251426
;  CURRENT APPLICATION NUMBER: US/10/381,752
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: PCT/US01/00432
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/174,513
```

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;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
;   LENGTH: 62
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-381-752-30

  Query Match             57.3%;  Score 217;  DB 12;  Length 62;
  Best Local Similarity   76.1%;  Pred. No. 1.5e-18;
  Matches   35;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         19 GDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSS 64
              ||:|||||||:| ||:| |||| | |||:| ||||||||||||||::
Db          1 GDVPPGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCCVSNT 46


RESULT 7
US-10-381-752-22
; Sequence 22, Application US/10381752
; Publication No. US20040072777A1
; GENERAL INFORMATION:
;  APPLICANT: Froehlich, Otto
;  APPLICANT:  Young, Leona G.
;  TITLE OF INVENTION: Epididymal Antimicrobial Peptides
;  FILE REFERENCE: 05501-0132US  43150-251426
;  CURRENT APPLICATION NUMBER: US/10/381,752
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: PCT/US01/00432
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/174,513
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
;   LENGTH: 64
;   TYPE: PRT
;   ORGANISM: Pan troglodytes
US-10-381-752-22

  Query Match             57.3%;  Score 217;  DB 12;  Length 64;
  Best Local Similarity   75.0%;  Pred. No. 1.5e-18;
  Matches   36;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         17 NSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSS 64
              ||||:| |||||:| ||:| |||| | |||:| ||||||||||||::
Db          1 NSGDVPLGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCCVSNT 48


RESULT 8
US-10-381-752-19
; Sequence 19, Application US/10381752
; Publication No. US20040072777A1
; GENERAL INFORMATION:
;  APPLICANT: Froehlich, Otto
;  APPLICANT:  Young, Leona G.
;  TITLE OF INVENTION: Epididymal Antimicrobial Peptides
;  FILE REFERENCE: 05501-0132US  43150-251426
;  CURRENT APPLICATION NUMBER: US/10/381,752
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: PCT/US01/00432
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/174,513
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-381-752-19

  Query Match             57.3%;  Score 217;  DB 12;  Length 109;
  Best Local Similarity   76.1%;  Pred. No. 2.6e-18;
  Matches   35;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         19 GDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSS 64
              ||:|||||||:| ||:| |||| | |||:| ||||||||||||||::
Db         48 GDVPPGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCCVSNT 93


RESULT 9
US-10-381-752-7
; Sequence 7, Application US/10381752
; Publication No. US20040072777A1
; GENERAL INFORMATION:
;  APPLICANT: Froehlich, Otto
;  APPLICANT:  Young, Leona G.
;  TITLE OF INVENTION: Epididymal Antimicrobial Peptides
;  FILE REFERENCE: 05501-0132US  43150-251426
;  CURRENT APPLICATION NUMBER: US/10/381,752
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: PCT/US01/00432
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/174,513
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
;   LENGTH: 133
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-381-752-7

  Query Match             57.3%;  Score 217;  DB 12;  Length 133;
  Best Local Similarity   76.1%;  Pred. No. 3.2e-18;
  Matches   35;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         19 GDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSS 64
              ||:|||||||:| ||:| |||| | |||:| ||||||||||||||::
Db         72 GDVPPGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCCVSNT 117


RESULT 10
US-10-381-752-31
; Sequence 31, Application US/10381752
; Publication No. US20040072777A1
; GENERAL INFORMATION:
;  APPLICANT: Froehlich, Otto
;  APPLICANT:  Young, Leona G.
;  TITLE OF INVENTION: Epididymal Antimicrobial Peptides
;  FILE REFERENCE: 05501-0132US  43150-251426
;  CURRENT APPLICATION NUMBER: US/10/381,752
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: PCT/US01/00432
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/174,513
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 62
;   TYPE: PRT
;   ORGANISM: Pan troglodytes
US-10-381-752-31

  Query Match             54.6%;  Score 207;  DB 12;  Length 62;
  Best Local Similarity   73.9%;  Pred. No. 2.4e-17;
  Matches   34;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         19 GDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSS 64
              ||:| |||||:| ||:| |||| | |||:| ||||||||||||::
Db          1 GDVPLGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCCVSNT 46
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RESULT 11
US-10-381-752-20
; Sequence 20, Application US/10381752
; Publication No. US20040072777A1
; GENERAL INFORMATION:
;  APPLICANT: Froehlich, Otto
;  APPLICANT:  Young, Leona G.
;  TITLE OF INVENTION: Epididymal Antimicrobial Peptides
;  FILE REFERENCE: 05501-0132US  43150-251426
;  CURRENT APPLICATION NUMBER: US/10/381,752
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: PCT/US01/00432
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/174,513
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Pan troglodytes
US-10-381-752-20

  Query Match             54.6%;  Score 207;  DB 12;  Length 109;
  Best Local Similarity   73.9%;  Pred. No. 4.2e-17;
  Matches   34;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         19 GDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSS 64
              ||:| |||||:| ||:| |||| | |||:| ||||||||||||::
Db         48 GDVPLGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCCVSNT 93


RESULT 12
US-10-381-752-8
; Sequence 8, Application US/10381752
; Publication No. US20040072777A1
; GENERAL INFORMATION:
;  APPLICANT: Froehlich, Otto
;  APPLICANT:  Young, Leona G.
;  TITLE OF INVENTION: Epididymal Antimicrobial Peptides
;  FILE REFERENCE: 05501-0132US  43150-251426
;  CURRENT APPLICATION NUMBER: US/10/381,752
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: PCT/US01/00432
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 60/174,513
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 69
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 133
;   TYPE: PRT
;   ORGANISM: Pan troglodytes
US-10-381-752-8

  Query Match             54.6%;  Score 207;  DB 12;  Length 133;
  Best Local Similarity   73.9%;  Pred. No. 5.1e-17;
  Matches   34;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         19 GDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVSSS 64
              ||:| |||||:| ||:| |||| | |||:| ||||||||||||::
Db         72 GDVPLGIRNTICRMQQGICRLFFCHSGEKKRDICSDPWNRCCVSNT 117


RESULT 13
US-10-252-734-25
; Sequence 25, Application US/10252734
; Publication No. US20030176652A1
; GENERAL INFORMATION:
;  APPLICANT: MCCRAY, JR., PAUL B.
;  APPLICANT:  SCHUTTE, BRIAN C.
;  APPLICANT:  JIA, HONG PENG
;  APPLICANT:  CASAVANT, THOMAS L.
;  TITLE OF INVENTION: HUMAN AND MOUSE b-DEFENSINS, ANTIMICROBIAL PEPTIDES
;  FILE REFERENCE: IOWA:041US
;  CURRENT APPLICATION NUMBER: US/10/252,734
;  CURRENT FILING DATE:  2002-09-23
;  PRIOR APPLICATION NUMBER: 60/323,991
;  PRIOR FILING DATE: 2001-09-21
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 35
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-252-734-25

  Query Match             52.0%;  Score 197;  DB 14;  Length 35;
  Best Local Similarity   94.1%;  Pred. No. 2.1e-16;
  Matches   32;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         28 TVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCV 61
              ||| ||:|||||||||||||||||||||||||||
Db          1 TVCLMQQGHCRLFMCRSGERKGDICSDPWNRCCV 34


RESULT 14
US-10-252-734-24
; Sequence 24, Application US/10252734
; Publication No. US20030176652A1
; GENERAL INFORMATION:
;  APPLICANT: MCCRAY, JR., PAUL B.
;  APPLICANT:  SCHUTTE, BRIAN C.
;  APPLICANT:  JIA, HONG PENG
;  APPLICANT:  CASAVANT, THOMAS L.
;  TITLE OF INVENTION: HUMAN AND MOUSE b-DEFENSINS, ANTIMICROBIAL PEPTIDES
;  FILE REFERENCE: IOWA:041US
;  CURRENT APPLICATION NUMBER: US/10/252,734
;  CURRENT FILING DATE:  2002-09-23
;  PRIOR APPLICATION NUMBER: 60/323,991
;  PRIOR FILING DATE: 2001-09-21
;  NUMBER OF SEQ ID NOS: 82
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 35
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-252-734-24

  Query Match             43.5%;  Score 165;  DB 14;  Length 35;
  Best Local Similarity   77.1%;  Pred. No. 1.4e-12;
  Matches   27;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy         28 TVCFMQRGHCRLFMCRSGERKGDICSDPWNRCCVS 62
              |:| ||:| |||| | |||:| |||||||||||||
Db          1 TICRMQQGICRLFFCHSGEKKRDICSDPWNRCCVS 35


RESULT 15
US-10-372-876-136
; Sequence 136, Application US/10372876
; Publication No. US20030204071A1
; GENERAL INFORMATION:
;  APPLICANT: Moore, Paul A. et al.
;  TITLE OF INVENTION: 110 Human Secreted Proteins
;  FILE REFERENCE: PZ021P1
;  CURRENT APPLICATION NUMBER: US/10/372,876
;  CURRENT FILING DATE:  2003-02-26
;  PRIOR APPLICATION NUMBER: 09/334,595
;  PRIOR FILING DATE: 1999-06-17
;  PRIOR APPLICATION NUMBER: PCT/US98/27059
;  PRIOR FILING DATE: 1998-12-17
;  PRIOR APPLICATION NUMBER: 60/070,923
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,007
;  PRIOR FILING DATE: 1997-12-18
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;  PRIOR APPLICATION NUMBER: 60/068,057
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,006
;  PRIOR FILING DATE: 1997-12-18
;  PRIOR APPLICATION NUMBER: 60/068,369
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/068,367
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/068,368
;  PRIOR FILING DATE: 1997-12-19
;  PRIOR APPLICATION NUMBER: 60/068,169
;  PRIOR FILING DATE: 1997-12-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 672
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 136
;   LENGTH: 124
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (124)
;   OTHER INFORMATION: Xaa equals stop translation
US-10-372-876-136

  Query Match             20.2%;  Score 76.5;  DB 12;  Length 124;
  Best Local Similarity   32.4%;  Pred. No. 0.22;
  Matches   22;  Conservative   10;  Mismatches   31;  Indels    5;  Gaps    3;

Qy          1 MKVLLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              ||:|||      |: :    ||       |: : ||||   |: ||   | | :    ||
Db          1 MKLLLLALPMLVLLPQ---VIPAYSGEKKCWNRSGHCRK-QCKDGEAVKDTCKN-LRACC 55

Qy         61 VSSSIKNR 68
              : |:  :|
Db         56 IPSNEDHR 63


Search completed: June 14, 2004, 16:46:23
Job time : 43 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 14, 2004, 16:36:35 ; Search time 21 Seconds
(without alignments)
311.477 Million cell updates/sec

Title: US-10-623-629-2
Perfect score: 379
Sequence: 1 MKVLLLFAVFFCLVQRNSGD.....GDICSDPWNRCCVSSSIKNR 68

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	67.5	17.8	65	2	C35947	crotamine 3 precur
2	64.5	17.0	276	2	T08773	hypothetical prote
3	63.5	16.8	40	2	I45495	beta-defensin-9 -
4	63	16.6	139	2	T34238	hypothetical prote
5	63	16.6	3635	2	T10053	laminin alpha 5 ch
6	62.5	16.5	40	2	G45495	beta-defensin-7 -
7	62.5	16.5	42	2	C45495	beta-defensin-3 -
8	62.5	16.5	118	2	I51574	gene wnt-6 protein
9	62.5	16.5	345	2	T25138	hypothetical prote
10	62.5	16.5	358	2	T25137	hypothetical prote
11	62	16.4	64	2	A56128	lingual antimicrob
12	62	16.4	139	2	T33138	hypothetical prote
13	62	16.4	205	2	H69889	hypothetical prote
14	60.5	16.0	34	2	I48887	cryptdin-4 - mouse
15	60.5	16.0	364	2	F36470	Wnt-6 protein - mo
16	60.5	16.0	365	2	JC7694	soluble-type glyco
17	60	15.8	575	1	VCLJHD	env polyprotein pr
18	59.5	15.7	65	2	A35947	crotamine 1 precur
19	59.5	15.7	378	2	B59180	Wnt inhibitory fac
20	59.5	15.7	555	2	A33723	Cypridina-luciferi
21	59	15.6	644	2	C70585	hypothetical prote
22	58	15.3	101	2	JQ0877	cyc02 protein prec
23	57.5	15.2	41	2	D45495	beta-defensin-4 -
24	57.5	15.2	94	1	A40499	defensin alpha-1 p
25	57.5	15.2	494	2	S57539	probable membrane
26	57.5	15.2	2471	2	A49128	cell-fate determin
27	57	15.0	139	2	T33137	hypothetical prote
28	57	15.0	2555	2	A40043	notch protein homo
29	56.5	14.9	116	2	T10084	lipid transfer pro
30	56.5	14.9	116	2	T10098	nonspecific lipid
31	56.5	14.9	261	2	A90926	hypothetical prote
32	56.5	14.9	261	2	E85774	hypothetical prote
33	56.5	14.9	261	2	F64924	probable thiosulfa
34	56.5	14.9	298	2	JC7568	kidney inhibitor o
35	56.5	14.9	337	2	A53041	effector cell prot
36	56.5	14.9	389	2	T29488	hypothetical prote
37	56.5	14.9	430	2	T18475	hypothetical prote
38	56.5	14.9	505	2	T10896	cytochrome P450 (E
39	56.5	14.9	996	2	JE0237	apolipoprotein E r
40	56.5	14.9	2229	2	T16199	hypothetical prote
41	56	14.8	227	1	LNRZ	lectin precursor -
42	56	14.8	258	2	A69805	hypothetical prote
43	56	14.8	491	2	JT0676	cytochrome P450 2B
44	56	14.8	664	2	T52121	acyl-CoA oxidase (
45	56	14.8	704	2	JC7881	ceramidase (EC 3.5

ALIGNMENTS

RESULT 1
C35947
crotamine 3 precursor - tropical rattlesnake
C;Species: Crotalus durissus terrificus (tropical rattlesnake, cascabel)
C;Date: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 24-Jun-1993
C;Accession: C35947
R;Smith, L.A.; Schmidt, J.J.
Toxicon 28, 575-585, 1990
A;Title: Cloning and nucleotide sequences of crotamine genes.
A;Reference number: A35947; MUID:90357261; PMID:2389256
A;Accession: C35947
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-65 <SMI>
C;Superfamily: crotamine

Query Match 17.8%; Score 67.5; DB 2; Length 65;
Best Local Similarity 34.6%; Pred. No. 0.64;
Matches 27; Conservative 3; Mismatches 23; Indels 25; Gaps 6;

```
Qy          1 MKVL-LLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDIC----SD- 54
              ||:| |||| |           ||     | :: |||          || ||    ||
Db          1 MKILYLLFAFLFLAFLSE-----PGNAYKRCHIKGGHC--------FPKGKICIPPSSDF 47

Qy         55 -----PWNR-CCVSSSIK 66
                  || | ||   | |
Db         48 GKMDCPWRRKCCKKGSGK 65
```

RESULT 2
T08773
hypothetical protein DKFZp586N041.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T08773
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16474
A;Accession: T08773
A;Molecule type: mRNA
A;Residues: 1-276 <OTT>
A;Cross-references: EMBL:AL050140
A;Experimental source: adult uterus; clone DKFZp586N041
C;Genetics:
A;Note: DKFZp586N041.1

Query Match 17.0%; Score 64.5; DB 2; Length 276;
Best Local Similarity 29.5%; Pred. No. 4.8;
Matches 18; Conservative 6; Mismatches 24; Indels 13; Gaps 2;

```
Qy          8 AVFFCL----------VQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPW 56
              | |:|:          |:   || |  | ||   : :  |   | | |   | |  : |
```

```
Db        179 ATFYCISMQWFREWESFVKGKDGDPPGPIDNTKIAVTK--CGNVMLRQGADSGQISEETW 236

Qy         57 N 57
              |
Db        237 N 237
```

RESULT 3
I45495
beta-defensin-9 - bovine
N;Alternate names: peptide BNBD-9
N;Contains: beta-defensin-8
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #text_change 22-Apr-1995
C;Accession: I45495; H45495
R;Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens
J. Biol. Chem. 268, 6641-6648, 1993
A;Title: Purification, primary structures, and antibacterial activities of beta-defensin
A;Reference number: A45495; MUID:93203264; PMID:8454635
A;Accession: I45495
A;Molecule type: protein
A;Residues: 1-40 <SEL>
A;Note: sequence modified after extraction from NCBI backbone
A;Accession: H45495
A;Molecule type: protein
A;Residues: 3-40 <SE2>
A;Note: sequence extracted from NCBI backbone (NCBIP:127958)
C;Keywords: pyroglutamic acid
F;1-40/Product: beta-defensin-9 #status experimental <MA1>
F;3-40/Product: beta-defensin-8 #status experimental <MA2>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;9-38,16-31,21-39/Disulfide bonds: #status predicted

  Query Match   16.8%; Score 63.5; DB 2; Length 40;
  Best Local Similarity   36.8%; Pred. No. 1.2;
  Matches   14; Conservative   4; Mismatches   19; Indels   1; Gaps   1;

```
Qy         24 GIRNTV-CFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              |:|| | | : || |     |     |:    |  |  :||
Db          2 GVRNFVTCRINRGFCVPIRCPGHRRQIGTCLGPQIKCC 39
```

RESULT 4
T34238
hypothetical protein F22A3.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jun-2000
C;Accession: T34238
R;Hallsworth, K.
submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F22A3.
A;Reference number: Z21492
A;Accession: T34238
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-139 <HAL>
A;Cross-references: EMBL:U41547; PIDN:AAA83197.1; CESP:F22A3.6
C;Genetics:
A;Gene: CESP:F22A3.6
A;Introns: 12/1; 49/3; 88/3; 107/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F22A3.6

  Query Match   16.6%; Score 63; DB 2; Length 139;
  Best Local Similarity   23.9%; Pred. No. 4;
  Matches   22; Conservative   12; Mismatches   28; Indels   30; Gaps   5;

```
Qy          1 MKVLLLFAV---------FFCLVQRNSGDIPPGIRNTVCFMQRG--HCRLFMCRSG---- 45
              :| ||| :|          |:  | ||  | |     | |  |   |  :  : |
Db          3 VKSLLLLSVAIAYVSADCLHCICMRESGCKPIG-----CHMDVGSLSCGYYQIKIGYYED 57

Qy         46 -----ERKGDICSDPWNRC-----CVSSSIKN 67
                  :: |:     | ||      | :: ::|
Db         58 CGQPTKKAGETTEAAWKRCADDLNCATTCVEN 89
```

RESULT 5
T10053
laminin alpha 5 chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2003
C;Accession: T10053
R;Miner, J.H.; Lewis, R.M.; Sanes, J.R.
submitted to the EMBL Data Library, November 1997
A;Reference number: Z16923
A;Accession: T10053
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3635 <MIN>
A;Cross-references: EMBL:U37501; NID:g2599231; PID:g2599232
C;Genetics:
A;Gene: Lama5
C;Keywords: basement membrane; cell binding; extracellular matrix
F;1888-1939/Domain: laminin-type EGF-like homology <LEG>
F;1942-1970/Domain: EGF homology <EGF>

  Query Match   16.6%; Score 63; DB 2; Length 3635;
  Best Local Similarity   43.3%; Pred. No. 64;
  Matches   13; Conservative   6; Mismatches   7; Indels   4; Gaps   2;

```
Qy         23 PGIRNTVCFMQRGHCRLFMCRSGERKGDIC 52
              ||: |::|  : | |    |||:|  :|| |
Db        469 PGVANSLCDPESGQC---MCRTG-FEGDRC 494
```

RESULT 6
G45495
beta-defensin-7 - bovine
N;Alternate names: peptide BNBD-7
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #text_change 25-Oct-1996
C;Accession: G45495
R;Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens
J. Biol. Chem. 268, 6641-6648, 1993
A;Title: Purification, primary structures, and antibacterial activities of beta-defensin
A;Reference number: A45495; MUID:93203264; PMID:8454635
A;Accession: G45495
A;Molecule type: protein
A;Residues: 1-40 <SEL>
A;Note: sequence modified after extraction from NCBI backbone
C;Keywords: antibacterial; disulfide bond; pyroglutamic acid
F;1-40/Product: beta-defensin-7 #status experimental <MA1>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;9-38,16-31,21-39/Disulfide bonds: #status predicted

  Query Match   16.5%; Score 62.5; DB 2; Length 40;
  Best Local Similarity   36.8%; Pred. No. 1.6;
  Matches   14; Conservative   4; Mismatches   19; Indels   1; Gaps   1;

```
Qy         24 GIRNTV-CFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              |:|| | | : || |     |     |:    |  |  :||
Db          2 GVRNFVTCRINRGFCVPIRCPGHRRQIGTCLGPRIKCC 39
```

RESULT 7
C45495
beta-defensin-3 - bovine
N;Alternate names: peptide BNBD-3
N;Contains: beta-defensin-2
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Feb-1994 #sequence_revision 22-Apr-1995 #text_change 25-Oct-1996
C;Accession: C45495; B45495
R;Selsted, M.E.; Tang, Y.Q.; Morris, W.L.; McGuire, P.A.; Novotny, M.J.; Smith, W.; Hens
J. Biol. Chem. 268, 6641-6648, 1993
A;Title: Purification, primary structures, and antibacterial activities of beta-defensin
A;Reference number: A45495; MUID:93203264; PMID:8454635
A;Accession: C45495

A;Molecule type: protein
A;Residues: 1-42 <SEL>
A;Note: sequence modified after extraction from NCBI backbone
A;Accession: B45495
A;Molecule type: protein
A;Residues: 3-42 <SE2>
A;Note: sequence extracted from NCBI backbone (NCBIP:127952)
C;Keywords: antibacterial; disulfide bond; pyroglutamic acid
F;1-42/Product: beta-defensin-3 #status experimental <MA1>
F;3-42/Product: beta-defensin-2 #status experimental <MA2>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;9-38,16-31,21-39/Disulfide bonds: #status predicted

  Query Match 16.5%; Score 62.5; DB 2; Length 42;
  Best Local Similarity 37.5%; Pred. No. 1.7;
  Matches 15; Conservative 4; Mismatches 20; Indels 1; Gaps 1;

Qy 24 GIRNTV-CFMQRGHCRLFMCRSGERKGDICSDPWNRCCVS 62
Db 2 GVRNHVTCRINRGFCVPIRCPGRTRQIGTCFGPRIKCCRS 41

RESULT 8
I51574
gene wnt-6 protein - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: I51574
R;Wolda, S.L.; Moon, R.T.
Oncogene 7, 1941-1947, 1992
A;Title: Cloning and developmental expression in Xenopus laevis of seven additional memb
A;Reference number: I51571; MUID:93026368; PMID:1408135
A;Accession: I51574
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-118 <WOL>
A;Cross-references: GB:L07532; NID:g214883; PIDN:AAA49985.1; PID:g214884
C;Genetics:
A;Gene: wnt-6
C;Superfamily: int-1 transforming protein

  Query Match 16.5%; Score 62.5; DB 2; Length 118;
  Best Local Similarity 36.6%; Pred. No. 4;
  Matches 15; Conservative 4; Mismatches 17; Indels 5; Gaps 2;

Qy 11 FCLVQRNSGDIPPGIRNTVC---FMQRGHCRLFMCRSGERK 48
Db 68 FCQANRKTGS--PGTRGRVCNSTALDVGGCDLLCCGRGQRE 106

RESULT 9
T25138
hypothetical protein T22H2.6b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Dec-2002
C;Accession: T25138
R;Lennard, N.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19985
A;Accession: T25138
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-345 <WIL>
A;Cross-references: EMBL:Z81595; PIDN:CAB54305.1; GSPDB:GN00019; CESP:T22H2.6b
A;Experimental source: clone T22H2
C;Genetics:
A;Gene: CESP:T22H2.6b
A;Map position: 1
A;Introns: 93/3; 232/3; 314/3
C;Superfamily: protein T22H2.6

  Query Match 16.5%; Score 62.5; DB 2; Length 345;
  Best Local Similarity 27.6%; Pred. No. 9.9;
  Matches 24; Conservative 9; Mismatches 25; Indels 29; Gaps 5;

Qy 1 MKVLLLF-AVFFCLVQRNS----------GDIPPG---IRNTVCFMQRGHCRLF 40
Db 79 MRLILLFLAVFLCRVTAHQCDAETECSDDETCCKLGDNTWGCCPMPNAVCCDDRSHC--- 135

Qy 41 MCRSGERKGDICSDPWNRCCVSSSIKN 67
Db 136 -CPTG-----TTCDPQGARCIGADEKH 156

RESULT 10
T25137
hypothetical protein T22H2.6a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Dec-2002
C;Accession: T25137
R;Lennard, N.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19985
A;Accession: T25137
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-358 <WIL>
A;Cross-references: EMBL:Z81595; PIDN:CAB54304.1; GSPDB:GN00019; CESP:T22H2.6a
A;Experimental source: clone T22H2
C;Genetics:
A;Gene: CESP:T22H2.6a
A;Map position: 1
A;Introns: 93/3; 232/3; 314/3
C;Superfamily: protein T22H2.6

  Query Match 16.5%; Score 62.5; DB 2; Length 358;
  Best Local Similarity 27.6%; Pred. No. 10;
  Matches 24; Conservative 9; Mismatches 25; Indels 29; Gaps 5;

Qy 1 MKVLLLF-AVFFCLVQRNS----------GDIPPG---IRNTVCFMQRGHCRLF 40
Db 79 MRLILLFLAVFLCRVTAHQCDAETECSDDETCCKLGDNTWGCCPMPNAVCCDDRSHC--- 135

Qy 41 MCRSGERKGDICSDPWNRCCVSSSIKN 67
Db 136 -CPTG-----TTCDPQGARCIGADEKH 156

RESULT 11
A56128
lingual antimicrobial peptide precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Nov-1999
C;Accession: A56128; B56128
R;Schonwetter, B.S.; Stolzenberg, E.D.; Zasloff, M.A.
Science 267, 1645-1648, 1995
A;Title: Epithelial antibiotics induced at sites of inflammation.
A;Reference number: A56128; MUID:95192714; PMID:7886453
A;Accession: A56128
A;Molecule type: mRNA
A;Residues: 1-64 <SCH>
A;Cross-references: GB:S76279; NID:g894208; PIDN:AAB33727.1; PID:g894209
A;Accession: B56128
A;Molecule type: protein
A;Residues: 23-64 <SC2>
C;Keywords: antibacterial; antifungal
F;1-20/Domain: signal sequence #status predicted <SIG>
F;23-64/Product: lingual antimicrobial peptide #status experimental <MAT>

  Query Match 16.4%; Score 62; DB 2; Length 64;
  Best Local Similarity 29.8%; Pred. No. 2.7;
  Matches 17; Conservative 8; Mismatches 30; Indels 2; Gaps 2;

Qy 5 LLFAVFFCLVQRNSGDIPPGIRNT-VCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
Db 6 LLLALLFLVLSAGSG-FTQGVRNSQSCRRNKGICVPIRCPGSMRQIGTCLGAQVKCC 61

RESULT 12
T33138
hypothetical protein C45G7.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 20-Jun-2000
C;Accession: T33138
R;Dante, M.; Wamsley, P.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid C45G7.
A;Reference number: Z21288
A;Accession: T33138
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-139 <DAN>
A;Cross-references: EMBL:AF067611; PIDN:AAC19181.1; GSPDB:GN00022; CESP:C45G7.2
A;Experimental source: strain Bristol N2; clone C45G7
C;Genetics:
A;Gene: CESP:C45G7.2
A;Map position: 4
A;Introns: 12/1; 49/3; 88/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F22A3.6

  Query Match   16.4%; Score 62; DB 2; Length 139;
  Best Local Similarity   21.8%; Pred. No. 5.2;
  Matches   19; Conservative   18; Mismatches   30; Indels   20; Gaps   4;

Qy   1 MKVLLLFAV---------FFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFM-----C-RSG 45
              :| :|| :: |: | || | | | : |: :: : | : |
Db   3 VKAILLLSIAVAYASADCLHCICMRESGCKPIGCHMDVGSLSCGYYQIKIPYYEDCGQPG 62

Qy   46 ERKGDICSDPWNRC-----CVSSSIKN 67
              :: |: | || | :: ::|
Db   63 KKHGESTEVAWKRCADDLKCATNCVEN 89

RESULT 13
H69889
hypothetical protein yndH - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: H69889
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: H69889
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-205 <KUN>
A;Cross-references: GB:Z99113; GB:AL009126; NID:g2634090; PIDN:CAB13663.1; PID:g2634163
A;Experimental source: strain 168
C;Genetics:
A;Gene: yndH
C;Superfamily: Bacillus subtilis hypothetical protein yndH

  Query Match   16.4%; Score 62; DB 2; Length 205;
  Best Local Similarity   27.1%; Pred. No. 7.3;
  Matches   16; Conservative   7; Mismatches   20; Indels   16; Gaps   2;

Qy   1 MKVLLLFAVFF-CLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNR 58
              :::|| ||| | ||| |:| | :: | : |||
Db   47 VRMLLKLGVFFRCFFSERGKDIPFTIQNRTCLLKSQHTGI--------------EWNR 90

RESULT 14
I48887
cryptdin-4 - mouse (fragment)
N;Alternate names: crypt defensin 4
C;Species: Mus musculus (house mouse)
C;Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 16-Jul-1999
C;Accession: I48887; D43279
R;Huttner, K.M.; Selsted, M.E.; Ouellette, A.J.
Genomics 19, 448-453, 1994
A;Title: Structure and diversity of the murine cryptdin gene family.
A;Reference number: A50017; MUID:94245232; PMID:8188287
A;Accession: I48887
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-34 <RES>
A;Cross-references: EMBL:U03032; NID:g437245; PIDN:AAA57172.1; PID:g437246
R;Selsted, M.E.; Miller, S.I.; Henschen, A.H.; Ouellette, A.J.
J. Cell Biol. 118, 929-936, 1992
A;Title: Enteric defensins: antibiotic peptide components of intestinal host defense.
A;Reference number: A43279; MUID:92363933; PMID:1500431
A;Accession: D43279
A;Molecule type: protein
A;Residues: 3-33 <SEL>
A;Experimental source: intestinal epithelium
A;Note: sequence extracted from NCBI backbone (NCBIP:110696)
C;Genetics:
A;Gene: Defcr4
C;Superfamily: mammalian defensin

  Query Match   16.0%; Score 60.5; DB 2; Length 34;
  Best Local Similarity   30.6%; Pred. No. 2.4;
  Matches   11; Conservative   7; Mismatches   13; Indels   5; Gaps   1;

Qy   25 IRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              :| :|: ::|| |: ||| | : ||
Db   1 LRGLLCYCRKGH-----CKRGERVRGTCGIRFLYCC 31

RESULT 15
F36470
Wnt-6 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Apr-1991 #sequence_revision 19-Apr-1991 #text_change 16-Jul-1999
C;Accession: F36470
R;Gavin, B.J.; McMahon, J.A.; McMahon, A.P.
Genes Dev. 4, 2319-2332, 1990
A;Title: Expression of multiple novel Wnt-1/int-1-related genes during fetal and adult m
A;Reference number: A36470; MUID:91122634; PMID:2279700
A;Accession: F36470
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-364 <GAV>
A;Cross-references: GB:M89800; NID:g202407; PIDN:AAA40569.1; PID:g202408
C;Superfamily: int-1 transforming protein

  Query Match   16.0%; Score 60.5; DB 2; Length 364;
  Best Local Similarity   30.0%; Pred. No. 18;
  Matches   21; Conservative   4; Mismatches   28; Indels   17; Gaps   5;

Qy   5 LLFAV---FFCLVQRNSGDIPPGIRNTVCFMQR---GHCRLFMCRSGERKGDI------- 51
              ||:| || | :| || | | | | | | | |: :
Db   283 LLYAADSPDFCAPNRRTGS--PGTRGRACNSSAPDLSGCDLLCCGRGHRQESVQLEENCL 340

Qy   52 CSDPWNRCCV 61
              | | |||
Db   341 CRFHW--CCV 348

Search completed: June 14, 2004, 16:41:13
Job time : 37 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 14, 2004, 16:29:44 ; Search time 14 Seconds
(without alignments)
252.912 Million cell updates/sec

Title: US-10-623-629-2
Perfect score: 379
Sequence: 1 MKVLLLFAVFFCLVQRNSGD.....GDICSDPWNRCCVSSSIKNR 68

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	76.5	20.2	123	1	D118_HUMAN	Q96ph6 homo sapien
2	75	19.8	63	1	BD04_BOVIN	P46162 bos taurus
3	74	19.5	88	1	D120_HUMAN	Q8n689 homo sapien
4	72	19.0	64	1	BD01_CAPHI	O97946 capra hircu
5	71.5	18.9	123	1	D118_MACMU	Q95li0 macaca mula
6	71	18.7	55	1	BD09_BOVIN	P46167 bos taurus
7	71	18.7	57	1	BD03_BOVIN	P46161 bos taurus
8	70	18.5	129	1	WNT6_XENLA	P31287 xenopus lae
9	69	18.2	64	1	BD01_SHEEP	O19038 ovis aries
10	68.5	18.1	87	1	NUOS_HUMAN	Q9nrx3 homo sapien
11	67.5	17.8	65	1	MYX3_CRODU	P24333 crotalus du
12	66	17.4	64	1	D103_PANTR	Q95jd2 pan troglod
13	66	17.4	64	1	EAP_BOVIN	O02775 bos taurus
14	66	17.4	67	1	D103_HUMAN	P81534 homo sapien
15	65.5	17.3	96	1	DEF1_MACMU	P60030 macaca mula
16	65	17.2	64	1	BD02_SHEEP	O19039 ovis aries
17	64.5	17.0	96	1	DEF3_MACMU	P60031 macaca mula
18	64.5	17.0	96	1	DEF8_MACMU	P60032 macaca mula
19	64.5	17.0	942	1	UB33_HUMAN	Q8tey7 homo sapien
20	63	16.6	3718	1	LMA5_MOUSE	Q61001 mus musculu
21	62.5	16.5	40	1	BD07_BOVIN	P46165 bos taurus
22	62.5	16.5	70	1	D131_HUMAN	P59861 homo sapien
23	62.5	16.5	117	1	WNT6_PLEJO	P28137 plethodon j
24	62	16.4	64	1	LAP_BOVIN	Q28880 bos taurus
25	60.5	16.0	92	1	DEF4_MOUSE	P28311 mus musculu
26	60.5	16.0	364	1	WNT6_MOUSE	P22727 mus musculu
27	60.5	16.0	365	1	WNT6_HUMAN	Q9y6f9 homo sapien
28	60	15.8	64	1	AMP2_MELGA	P80392 meleagris g
29	60	15.8	64	1	GLL3_CHICK	P46158 gallus gall
30	60	15.8	575	1	ENV_SMRVH	P21412 squirrel mo
31	59.5	15.7	65	1	MYX1_CRODU	P24331 crotalus du
32	59.5	15.7	378	1	WIF1_BRARE	Q9w6f9 brachydanio
33	59.5	15.7	555	1	LUCI_VARHI	P17554 vargula hil
34	59.5	15.7	1242	1	JAG1_BRARE	Q90y57 brachydanio
35	58	15.3	101	1	CY02_CATRO	P25923 catharanthu
36	57.5	15.2	38	1	BD08_BOVIN	P46166 bos taurus
37	57.5	15.2	94	1	DEF1_HUMAN	P59665 homo sapien
38	57.5	15.2	1218	1	JAG1_HUMAN	P78504 homo sapien
39	57.5	15.2	2471	1	NTC2_RAT	Q9qw30 rattus norv
40	57	15.0	2556	1	NTC1_HUMAN	P46531 homo sapien
41	56.5	14.9	40	1	BD02_BOVIN	P46160 bos taurus
42	56.5	14.9	116	1	NLTC_RICCO	P10975 ricinus com
43	56.5	14.9	117	1	WNT6_THUTH	P28145 thunnus thy
44	56.5	14.9	147	1	PA22_BUNCE	Q8qfw3 bungarus ca
45	56.5	14.9	261	1	PHSC_ECOLI	P77409 escherichia

ALIGNMENTS

RESULT 1
D118_HUMAN
ID D118_HUMAN STANDARD; PRT; 123 AA.
AC Q96PH6; Q8N691; Q9NUH0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Beta-defensin 118 precursor (Beta-defensin 18) (DEFB-18) (Epididymal
DE secretory protein 13.6) (ESP13.6).
GN DEFB118 OR DEFB18 OR ESC42 OR C20ORF63.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Epididymis;
RX MEDLINE=21448442; PubMed=11564719;
RA Liu Q., Hamil K.G., Sivashanmugnam P., Grossman G., Soundararajan R.,
RA Rao A.J., Richardson R.T., Zhang Y.-L., O'Rand M.G., Petrusz P.,
RA French F.S., Hall S.H.;
RT "Primate epididymis-specific proteins: characterization of ESC42, a
RT novel protein containing a trefoil-like motif in monkey and human.";
RL Endocrinology 142:4529-4539(2001).
RN [2]
RP SEQUENCE FROM N.A., AND TISSUE DISTRIBUTION.
RX MEDLINE=22705149; PubMed=12600824;
RA Kao C.Y., Chen Y., Zhao Y.H., Wu R.;
RT "ORFeome-based search of airway epithelial cell-specific novel human
RT beta-defensin genes.";
RL Am. J. Respir. Cell Mol. Biol. 29:71-80(2003).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Lehvaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,

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RA   Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA   Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA   Rogers J.;
RT   "The DNA sequence and comparative analysis of human chromosome 20.";
RL   Nature 414:865-871(2001).
RN   [4]
RP   SEQUENCE OF 23-123 FROM N.A., AND IDENTIFICATION.
RC   TISSUE=B-cell, Fetal lung, and Testis;
RX   MEDLINE=21843921; PubMed=11854508;
RA   Schutte B.C., Mitros J.P., Bartlett J.A., Walters J.D., Jia H.P.,
RA   Welsh M.J., Casavant T.L., McCray P.B. Jr.;
RT   "Discovery of five conserved beta-defensin gene clusters using a
RT   computational search strategy.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:2129-2133(2002).
CC   -!- FUNCTION: Has antibacterial activity (Potential).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: High-level and epididymis-specific expression.
CC       Most abundant in the epithelium of the caput and is also present
CC       in the lumen and bound to sperm. Expressed also in pancreas.
CC   -!- SIMILARITY: Belongs to the beta-defensin family.
CC   -!- CAUTION: Ref.2 sequence differs from that shown due to erroneous
CC       gene model prediction.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF347073; AAL27987.1; -.
DR   EMBL; AF529415; AAQ09524.1; -.
DR   EMBL; AL031650; CAB72350.2; ALT_SEQ.
DR   EMBL; AY122471; AAM93913.1; -.
DR   Genew; HGNC:16196; DEFB118.
DR   MIM; 607650; -.
DR   GO; GO:0005653; C:perinuclear space; NAS.
DR   GO; GO:0003797; F:antibacterial peptide activity; TAS.
DR   GO; GO:0007160; P:cell-matrix adhesion; NAS.
DR   GO; GO:0045087; P:innate immune response; TAS.
DR   GO; GO:0007283; P:spermatogenesis; NAS.
KW   Antibiotic; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20     62       BETA-DEFENSIN 118.
FT   PROPEP       65    123       POTENTIAL.
FT   DISULFID     27     54       BY SIMILARITY.
FT   DISULFID     34     48       BY SIMILARITY.
FT   DISULFID     38     55       BY SIMILARITY.
SQ   SEQUENCE   123 AA;  13613 MW;  0CBAFDB0AE459BA6 CRC64;

  Query Match             20.2%;  Score 76.5;  DB 1;  Length 123;
  Best Local Similarity   32.4%;  Pred. No. 0.023;
  Matches   22;  Conservative   10;  Mismatches   31;  Indels    5;  Gaps    3;

Qy          1 MKVLLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              ||:|||      |: :    ||        |: : ||||   |: ||   | | :    ||
Db          1 MKLLLLALPMLVLLPQ---VIPAYSGEKKCWNRSGHCRK-QCKDGEAVKDTCKN-LRACC 55

Qy         61 VSSSIKNR 68
              : |:  :|
Db         56 IPSNEDHR 63


RESULT 2
BD04_BOVIN
ID   BD04_BOVIN     STANDARD;      PRT;    63 AA.
AC   P46162;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Beta-defensin 4 precursor (BNDB-4) (BNBD-4).
GN   DEFB4 OR BNBD4.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yount N.Y., Yuan J., Diamond G., Tarver A., McGuire P.A.,
RA   McCullough C., Cullor J.S., Bevins C.L., Selsted M.E.;
RT   "Molecular cloning and expression of an antimicrobial beta-defensin
RT   from bovine neutrophils. Characterization of BNBD-4 cDNA and genomic
RT   sequences and localization of the peptide to large granules of mature
RT   neutrophils.";
RL   Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Yount N.Y., Yuan J., Tarver A.P., Diamond G., Levy J.N.,
RA   McGuire P.A., McCullough C., Cullor J.S., Bevins C.L., Selsted M.E.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Yount N.Y., Yuan J., Tarver A.P., Diamond G., Levy J.N., McGuire P.A.,
RA   McCullough C., Cullor J.S., Bevins C.L., Selsted M.E.;
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Ryan L.K., Rhodes J., Bhat M., Diamond G.;
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 23-63.
RC   STRAIN=Hereford; TISSUE=Neutrophils;
RX   MEDLINE=93203264; PubMed=8454635;
RA   Selsted M.E., Tang Y.-Q., Morris W.L., McGuire P.A., Novotny M.J.,
RA   Smith W., Henschen A.H., Cullor J.S.;
RT   "Purification, primary structures, and antibacterial activities of
RT   beta-defensins, a new family of antimicrobial peptides from bovine
RT   neutrophils.";
RL   J. Biol. Chem. 268:6641-6648(1993).
CC   -!- FUNCTION: Has bactericidal activity. Active against E.coli ML35
CC       and S.aureus 502A.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Neutrophilic granules.
CC   -!- SIMILARITY: Belongs to the beta-defensin family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U36200; AAD10283.1; -.
DR   EMBL; AF008307; AAB63292.1; -.
DR   EMBL; AF014107; AAD01522.1; -.
DR   HSSP; P46170; 1BNB.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Antibiotic; Signal; Pyrrolidone carboxylic acid.
FT   SIGNAL        1     22
FT   CHAIN        23     63       BETA-DEFENSIN 4.
FT   MOD_RES      23     23       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     31     60       BY SIMILARITY.
FT   DISULFID     38     53       BY SIMILARITY.
FT   DISULFID     43     61       BY SIMILARITY.
SQ   SEQUENCE   63 AA;  7161 MW;  3A4427EF57D654A3 CRC64;

  Query Match             19.8%;  Score 75;  DB 1;  Length 63;
  Best Local Similarity   36.8%;  Pred. No. 0.018;
  Matches   21;  Conservative    5;  Mismatches   29;  Indels    2;  Gaps    2;
```

```
Qy          5 LLFAVFFCLVQRNSGDIPPGIRN-TVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              || || | ::    ||    :||   |    | |  |:|| | |:   |  |   ||
Db          6 LLLAVLFLVLSAGSG-FTQRVRNPQSCRWNMGVCIPFLCRVGMRQIGTCFGPRVPCC 61


RESULT 3
D120_HUMAN
ID   D120_HUMAN     STANDARD;      PRT;    88 AA.
AC   Q8N689;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Beta-defensin 120 precursor (Beta-defensin 20) (DEFB-20).
GN   DEFB120 OR DEFB20.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND IDENTIFICATION.
RC   TISSUE=B-cell, Fetal lung, and Testis;
RX   MEDLINE=21843921; PubMed=11854508;
RA   Schutte B.C., Mitros J.P., Bartlett J.A., Walters J.D., Jia H.P.,
RA   Welsh M.J., Casavant T.L., McCray P.B. Jr.;
RT   "Discovery of five conserved beta-defensin gene clusters using a
RT   computational search strategy.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:2129-2133(2002).
CC   -!- FUNCTION: Has antibacterial activity (Potential).
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- SIMILARITY: Belongs to the beta-defensin family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY122473; AAM93915.1; -.
DR   Genew; HGNC:18100; DEFB120.
KW   Antibiotic; Signal.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21     88       BETA-DEFENSIN 120.
FT   DISULFID     23     49       BY SIMILARITY.
FT   DISULFID     29     43       BY SIMILARITY.
FT   DISULFID     33     50       BY SIMILARITY.
SQ   SEQUENCE   88 AA;  10107 MW;  BFFFB1573ACF71C7 CRC64;

  Query Match             19.5%;  Score 74;  DB 1;  Length 88;
  Best Local Similarity   33.3%;  Pred. No. 0.033;
  Matches   21;  Conservative    9;  Mismatches   23;  Indels   10;  Gaps    4;

Qy          1 MKVLLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              ||:| ||      ::         : :  |:|  ||||| :|: ||     | :   |||
Db          1 MKLLYLFLAILLAIEE-------PVISVECWMD-GHCRL-LCKDGEDSIIRCRNR-KRCC 50

Qy         61 VSS 63
              | |
Db         51 VPS 53


RESULT 4
BD01_CAPHI
ID   BD01_CAPHI     STANDARD;      PRT;    64 AA.
AC   O97946;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Beta-defensin 1 precursor (BD-1).
GN   DEFB1.
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Capra.
OX   NCBI_TaxID=9925;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Tongue;
RX   MEDLINE=20002622; PubMed=10531296;
RA   Zhao C., Nguyen T., Liu L., Shamova O., Brogden K., Lehrer R.I.;
RT   "Differential expression of caprine beta-defensins in digestive and
RT   respiratory tissues.";
RL   Infect. Immun. 67:6221-6224(1999).
CC   -!- FUNCTION: Has bactericidal activity (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the beta-defensin family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y17679; CAA76811.1; -.
DR   HSSP; P46170; 1BNB.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Antibiotic; Signal.
FT   SIGNAL        1     20       POTENTIAL.
FT   PROPEP       21     26       POTENTIAL.
FT   CHAIN        27     64       BETA-DEFENSIN 1.
FT   DISULFID     31     60       BY SIMILARITY.
FT   DISULFID     38     53       BY SIMILARITY.
FT   DISULFID     43     61       BY SIMILARITY.
SQ   SEQUENCE   64 AA;  7258 MW;  492B824C8F57B042 CRC64;

  Query Match             19.0%;  Score 72;  DB 1;  Length 64;
  Best Local Similarity   33.3%;  Pred. No. 0.042;
  Matches   19;  Conservative    7;  Mismatches   29;  Indels    2;  Gaps    2;

Qy          5 LLFAVFFCLVQRNSGDIPPGIRN-TVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              ||  :|| ::   ||    |||:   |   :| | |  |    |:   | |  :||
Db          6 LLLVLFFLVLSAGSG-FTQGIRSRRSCHRNKGVCALTRCPRNMRQIGTCFGPPVKCC 61


RESULT 5
D118_MACMU
ID   D118_MACMU     STANDARD;      PRT;   123 AA.
AC   Q95LI0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Beta-defensin 118 precursor (Epididymal secretory protein 13.6)
DE   (ESP13.6).
GN   DEFB118 OR ESC42.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Epididymis;
RX   MEDLINE=21448442; PubMed=11564719;
RA   Liu Q., Hamil K.G., Sivashanmugam P., Grossman G., Soundararajan R.,
RA   Rao A.J., Richardson R.T., Zhang Y.L., O'Rand M.G., Petrusz P.,
RA   French F.S., Hall S.H.;
RT   "Primate epididymis-specific proteins: characterization of ESC42, a
RT   novel protein containing a trefoil-like motif in monkey and human.";
RL   Endocrinology 142:4529-4539(2001).
CC   -!- FUNCTION: Has antibacterial activity (Potential).
```

```
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: High-level and epdidymis-specific expression.
CC       Most abundant in the epithelium of the caput and is also present
CC       in the lumen and bound to sperm.
CC   -!- SIMILARITY: Belongs to the beta-defensin family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF207834; AAL26779.1; -.
DR   GO; GO:0005653; C:perinuclear space; NAS.
DR   GO; GO:0003797; F:antibacterial peptide activity; TAS.
DR   GO; GO:0007160; P:cell-matrix adhesion; NAS.
DR   GO; GO:0045087; P:innate immune response; TAS.
DR   GO; GO:0007283; P:spermatogenesis; NAS.
KW   Antibiotic; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20     62       BETA-DEFENSIN 118.
FT   PROPEP       65    123       POTENTIAL.
FT   DISULFID     27     54       BY SIMILARITY.
FT   DISULFID     34     48       BY SIMILARITY.
FT   DISULFID     38     55       BY SIMILARITY.
SQ   SEQUENCE   123 AA;  13629 MW;  EB0EF33715FF94E1 CRC64;

  Query Match             18.9%;  Score 71.5;  DB 1;  Length 123;
  Best Local Similarity   32.4%;  Pred. No. 0.092;
  Matches   22;  Conservative   10;  Mismatches   31;  Indels    5;  Gaps    3;

Qy          1 MKVLLLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              ||:|||      |: :    ||       |: : ||||   |: ||   : | :    ||
Db          1 MKLLLLALPILVLLPQ---VIPAYGGEKKCWNRSGHCRK-QCKDGEAVKETCKN-HRACC 55

Qy         61 VSSSIKNR 68
              | |:  :|
Db         56 VPSNEDHR 63


RESULT 6
BD09_BOVIN
ID   BD09_BOVIN     STANDARD;      PRT;    55 AA.
AC   P46167; O18814;
DT   01-NOV-1995 (Rel. 32, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Beta-defensin 9 precursor (BNDB-9) (BNBD-9) (Fragment).
GN   DEFB9 OR BNDB9.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Small intestine;
RX   MEDLINE=98147718; PubMed=9488394;
RA   Tarver A.P., Clark D.P., Diamond G., Russell J.P.,
RA   Erdjument-Bromage H., Tempst P., Cohen K.S., Jones D.E., Sweeney R.W.,
RA   Wines M., Hwang S., Bevins C.L.;
RT   "Enteric beta-defensin: molecular cloning and characterization of a
RT   gene with inducible intestinal epithelial cell expression associated
RT   with Cryptosporidium parvum infection.";
RL   Infect. Immun. 66:1045-1056(1998).
RN   [2]
RP   SEQUENCE OF 16-55.
RC   STRAIN=Hereford; TISSUE=Neutrophils;
RX   MEDLINE=93203264; PubMed=8454635;
RA   Selsted M.E., Tang Y.-Q., Morris W.L., McGuire P.A., Novotny M.J.,
RA   Smith W., Henschen A.H., Cullor J.S.;
RT   "Purification, primary structures, and antibacterial activities of
RT   beta-defensins, a new family of antimicrobial peptides from bovine
RT   neutrophils.";
RL   J. Biol. Chem. 268:6641-6648(1993).
CC   -!- FUNCTION: Has bactericidal activity. Active against E.coli ML35
CC       and S.aureus 502A.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Neutrophilic granules.
CC   -!- SIMILARITY: Belongs to the beta-defensin family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF016394; AAC48801.1; -.
DR   HSSP; P46170; 1BNB.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Antibiotic; Signal; Pyrrolidone carboxylic acid.
FT   NON_TER       1      1
FT   SIGNAL       <1      ?       POTENTIAL.
FT   PROPEP        ?     15       POTENTIAL.
FT   CHAIN        16     55       BETA-DEFENSIN 9.
FT   MOD_RES      16     16       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     24     53       BY SIMILARITY.
FT   DISULFID     31     46       BY SIMILARITY.
FT   DISULFID     36     54       BY SIMILARITY.
FT   CONFLICT     48     48       A -> G (IN REF. 2).
SQ   SEQUENCE   55 AA;  6049 MW;  48DAE6917DE366F2 CRC64;

  Query Match             18.7%;  Score 71;  DB 1;  Length 55;
  Best Local Similarity   33.3%;  Pred. No. 0.048;
  Matches   18;  Conservative    7;  Mismatches   27;  Indels    2;  Gaps    2;

Qy          8 AVFFCLVQRNSGDIPPGIRNTV-CFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              |: | ::   ||    |:|| | | : || |    |    |:   |  | :||
Db          2 ALLFLVLSAGSG-FTQGVRNFVTCRINRGFCVPIRCPGHRRQIGTCLAPQIKCC 54


RESULT 7
BD03_BOVIN
ID   BD03_BOVIN     STANDARD;      PRT;    57 AA.
AC   P46161;
DT   01-NOV-1995 (Rel. 32, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Beta-defensin 3 precursor (BNDB-3) (BNBD-3) (Fragment).
GN   DEFB3 OR BNDB3.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Small intestine;
RX   MEDLINE=98147718; PubMed=9488394;
RA   Tarver A.P., Clark D.P., Diamond G., Russell J.P.,
RA   Erdjument-Bromage H., Tempst P., Cohen K.S., Jones D.E., Sweeney R.W.,
RA   Wines M., Hwang S., Bevins C.L.;
RT   "Enteric beta-defensin: molecular cloning and characterization of a
RT   gene with inducible intestinal epithelial cell expression associated
RT   with Cryptosporidium parvum infection.";
RL   Infect. Immun. 66:1045-1056(1998).
RN   [2]
RP   SEQUENCE OF 15-67.
RC   STRAIN=Hereford; TISSUE=Neutrophils;
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RX   MEDLINE=93203264; PubMed=8454635;
RA   Selsted M.E., Tang Y.-Q., Morris W.L., McGuire P.A., Novotny M.J.,
RA   Smith W., Henschen A.H., Cullor J.S.;
RT   "Purification, primary structures, and antibacterial activities of
RT   beta-defensins, a new family of antimicrobial peptides from bovine
RT   neutrophils.";
RL   J. Biol. Chem. 268:6641-6648(1993).
CC   -!- FUNCTION: Has bactericidal activity. Active against E.coli ML35
CC       and S.aureus 502A.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Neutrophilic granules.
CC   -!- SIMILARITY: Belongs to the beta-defensin family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF016396; AAC48803.1; -.
DR   HSSP; P46170; 1BNB.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Antibiotic; Signal; Pyrrolidone carboxylic acid.
FT   NON_TER       1      1
FT   SIGNAL       <1      ?       POTENTIAL.
FT   PROPEP        ?     15       POTENTIAL.
FT   CHAIN        16     57       BETA-DEFENSIN 3.
FT   MOD_RES      16     16       PYRROLIDONE CARBOXYLIC ACID.
FT   DISULFID     24     53       BY SIMILARITY.
FT   DISULFID     31     46       BY SIMILARITY.
FT   DISULFID     36     54       BY SIMILARITY.
SQ   SEQUENCE   57 AA;  6324 MW;  835CA5828E33F7C1 CRC64;

  Query Match             18.7%;  Score 71;  DB 1;  Length 57;
  Best Local Similarity   33.9%;  Pred. No. 0.049;
  Matches   19;  Conservative    7;  Mismatches   28;  Indels    2;  Gaps    2;

Qy          8 AVFFCLVQRNSGDIPPGIRNTV-CFMQRGHCRLFMCRSGERKGDICSDPWNRCCVS 62
              |: | ::   ||    |:|| | | : || |    |    |:   |  |  :|| |
Db          2 ALLFLVLSAGSG-FTQGVRNHVTCRINRGFCVPIRCPGRTRQIGTCFGPRIKCCRS 56


RESULT 8
WNT6_XENLA
ID   WNT6_XENLA     STANDARD;      PRT;   129 AA.
AC   P31287;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Wnt-6 protein (XWnt-6) (Fragment).
GN   WNT-6.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93026368; PubMed=1408135;
RA   Wolda S.L., Moon R.T.;
RT   "Cloning and developmental expression in Xenopus laevis of seven
RT   additional members of the Wnt family.";
RL   Oncogene 7:1941-1947(1992).
CC   -!- FUNCTION: Ligand for members of the frizzled family of seven
CC       transmembrane receptors. Probable developmental protein. May be a
CC       signaling molecule which affects the development of discrete
CC       regions of tissues. Is likely to signal over only few cell
CC       diameters.
CC   -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC       extracellular matrix.
CC   -!- TISSUE SPECIFICITY: AT TAILBUD: DORSAL, PUNCTATE; IN ALDUT: BRAIN
CC       AND HEART.
CC   -!- DEVELOPMENTAL STAGE: GASTRULA ONWARDS.
CC   -!- SIMILARITY: Belongs to the Wnt family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; L07532; AAA49985.1; -.
DR   InterPro; IPR005817; Wnt.
DR   InterPro; IPR005816; Wnt_grthfactor.
DR   Pfam; PF00110; wnt; 1.
DR   PRINTS; PR01349; WNTPROTEIN.
DR   SMART; SM00097; WNT1; 1.
DR   PROSITE; PS00246; WNT1; 1.
KW   Wnt signaling pathway; Developmental protein; Glycoprotein.
FT   NON_TER       1      1
FT   CARBOHYD     92     92       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14260 MW;  FA7B61E918A9CE93 CRC64;

  Query Match             18.5%;  Score 70;  DB 1;  Length 129;
  Best Local Similarity   31.7%;  Pred. No. 0.15;
  Matches   19;  Conservative    5;  Mismatches   22;  Indels   14;  Gaps    4;

Qy         11 FCLVQRNSGDIPPGIRNTVC---FMQRGHCRLFMCRSGERKGDI-------CSDPWNRCC 60
              ||   | :|   || |  ||     :  | | |  |  |:|:  :       |   |  ||
Db         74 FCQANRKTGS--PGTRGRVCNSTALDVGGCDLLCCGRGQREETVVVEENCLCRFHW--CC 129


RESULT 9
BD01_SHEEP
ID   BD01_SHEEP     STANDARD;      PRT;    64 AA.
AC   O19038;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Beta-defensin 1 precursor (BD-1) (sBD1).
GN   DEFB1.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98138497; PubMed=9478010;
RA   Huttner K.M., Brezinski-Caliguri D.J., Mahoney M.M., Diamond G.;
RT   "Antimicrobial peptide expression is developmentally regulated in the
RT   ovine gastrointestinal tract.";
RL   J. Nutr. 128:297S-299S(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Trachea;
RX   MEDLINE=98121317; PubMed=9461419;
RA   Huttner K.M., Lambeth M.R., Burkin H.R., Broad T.E.;
RT   "Localization and genomic organization of sheep antimicrobial peptides
RT   genes.";
RL   Gene 206:85-91(1998).
CC   -!- FUNCTION: Has bactericidal activity (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- SIMILARITY: Belongs to the beta-defensin family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; U75250; AAB61995.1; -.
DR   HSSP; P46170; 1BNB.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Antibiotic; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23     64       BETA-DEFENSIN 1.
FT   DISULFID     31     60       BY SIMILARITY.
FT   DISULFID     38     53       BY SIMILARITY.
FT   DISULFID     43     61       BY SIMILARITY.
SQ   SEQUENCE   64 AA;  7244 MW;  3529A9B76ABD023A CRC64;

  Query Match             18.2%;  Score 69;  DB 1;  Length 64;
  Best Local Similarity   31.6%;  Pred. No. 0.096;
  Matches   18;  Conservative    8;  Mismatches   29;  Indels    2;  Gaps    2;

Qy          5 LLFAVFFCLVQRNSGDIPPGIRNTV-CFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              ||  :|| ::   ||    |:|| : |  :| |    |    |:   |  | :||
Db          6 LLLVLFFVVLSAGSG-FTQGVRNRLSCHRNKGVCVPSRCPRHMRQIGTCRGPPVKCC 61


RESULT 10
NUOS_HUMAN
ID   NUOS_HUMAN     STANDARD;      PRT;    87 AA.
AC   Q9NRX3;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   NADH:ubiquinone oxidoreductase MLRQ subunit homolog (NUOMS).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Adrenal gland;
RX   MEDLINE=20402571; PubMed=10931946;
RA   Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,
RA   Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,
RA   Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J.,
RA   Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M.,
RA   Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;
RT   "Gene expression profiling in the human hypothalamus-pituitary-adrenal
RT   axis and full-length cDNA cloning.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SIMILARITY: Belongs to the complex I NDUFA4 subunit family.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; AF164796; AAF80760.1; -.
DR   EMBL; BC011910; AAH11910.1; -.
SQ   SEQUENCE   87 AA;  9966 MW;  A08D7182A0A3CA87 CRC64;

  Query Match             18.1%;  Score 68.5;  DB 1;  Length 87;
  Best Local Similarity   29.9%;  Pred. No. 0.15;
  Matches   20;  Conservative   11;  Mismatches   27;  Indels    9;  Gaps    3;

Qy          6 LFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDICSD------PWNRC 59
              | | |:  ::|: | ||  :   :| : |   |:: |   |  |:| |      ||||
Db          6 LGARFYRQIKRHPGIIP--MIGLIC-LGMGSAALYLLRLALRSPDVCWDRKNNPEPWNRL 62

Qy         60 CVSSSIK 66
                :  |
Db         63 SPNDQYK 69


RESULT 11
MYX3_CRODU
ID   MYX3_CRODU     STANDARD;      PRT;    65 AA.
AC   P24333;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Myotoxin 3 precursor (Crotamine 3).
OS   Crotalus durissus terrificus (South American rattlesnake).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Viperidae; Crotalinae; Crotalus.
OX   NCBI_TaxID=8732;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RX   MEDLINE=90357261; PubMed=2389256;
RA   Smith L.A., Schmidt J.J.;
RT   "Cloning and nucleotide sequences of crotamine genes.";
RL   Toxicon 28:575-585(1990).
CC   -!- FUNCTION: Causes severe muscle necrosis by a non-enzymatic
CC       mechanism. Acts extremely rapidly and serves two primary
CC       functions: limit the flight of prey by causing instantaneous
CC       paralysis of the hind limbs and promote rapid death by paralysis
CC       of the diaphragm.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC   -!- SIMILARITY: Belongs to the snake toxin myotoxin family.
DR   PIR; C35947; C35947.
DR   InterPro; IPR000881; Myotoxin.
DR   Pfam; PF00819; Myotoxins; 1.
DR   PRINTS; PR00283; MYOTOXIN.
DR   ProDom; PD005972; Myotoxin; 1.
DR   PROSITE; PS00459; MYOTOXINS; 1.
KW   Toxin; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23     64       MYOTOXIN 3.
FT   DISULFID     26     58       BY SIMILARITY.
FT   DISULFID     33     52       BY SIMILARITY.
FT   DISULFID     40     59       BY SIMILARITY.
SQ   SEQUENCE   65 AA;  7371 MW;  A1B75A6CC515BA06 CRC64;

  Query Match             17.8%;  Score 67.5;  DB 1;  Length 65;
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  Best Local Similarity   34.6%;  Pred. No. 0.15;
  Matches   27;  Conservative    3;  Mismatches   23;  Indels   25;  Gaps    6;

Qy          1 MKVL-LLFAVFFCLVQRNSGDIPPGIRNTVCFMQRGHCRLFMCRSGERKGDIC----SD- 54
              ||:| |||| |          ||     | :: |||          || ||    ||
Db          1 MKILYLLFAFLFLAFLSE-----PGNAYKRCHIKGGHC--------FPKGKICIPPSSDF 47

Qy         55 -----PWNR-CCVSSSIK 66
                   || | ||   | |
Db         48 GKMDCPWRRKCCKKGSGK 65


RESULT 12
D103_PANTR
ID   D103_PANTR     STANDARD;      PRT;    64 AA.
AC   Q95JD2;
DT   15-MAR-2004 (Rel. 43, Created)
DT   15-MAR-2004 (Rel. 43, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Beta-defensin 103 precursor (Beta-defensin 3) (DEFB-3) (BD-3)
DE   (Fragment).
GN   DEFB103 OR DEFB3.
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skin;
RA   Duits L.A., Langermans J.A.M., Ravensbergen B., Paltansing S.,
RA   Vervenne R.A.W., Hiemstra P.S., Thomas A.W., Nibbering P.H.;
RT   "Expression of chimpanzee (Pan troglodytes) beta-defensin-3.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Exhibits antimicrobial activity against Gram-positive
CC       and Gram-negative bacteria (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the beta-defensin family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AY033883; AAK61549.1; -.
DR   InterPro; IPR001855; Defensin_beta.
DR   Pfam; PF00711; Defensin_beta; 1.
KW   Antibiotic; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    >64       BETA-DEFENSIN 103.
FT   DISULFID     33     62       BY SIMILARITY.
FT   DISULFID     40     55       BY SIMILARITY.
FT   DISULFID     45     63       BY SIMILARITY.
FT   NON_TER      64     64
SQ   SEQUENCE   64 AA;  7299 MW;  01C90D4B60218DC8 CRC64;

  Query Match             17.4%;  Score 66;  DB 1;  Length 64;
  Best Local Similarity   31.7%;  Pred. No. 0.22;
  Matches   19;  Conservative    8;  Mismatches   27;  Indels    6;  Gaps    2;

Qy          5 LLFAVFFCLVQRNSGDIPPGIRNTV----CFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              ||||: |  :    |    || ||:    | :: | | :  |   | :   ||    :||
Db          6 LLFALLFLFLVPVPGH--GGIINTLQKYYCRVRGGRCAVLTCLPKEEQIGKCSTRGRKCC 63


RESULT 13
EAP_BOVIN
ID   EAP_BOVIN      STANDARD;      PRT;    64 AA.
AC   O02775;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Enteric beta-defensin precursor.
GN   EBD.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98147718; PubMed=9488394;
RA   Tarver A.P., Clark D.P., Diamond G., Russell J.P.,
RA   Erdjument-Bromage H., Tempst P., Cohen K.S., Jones D.E., Sweeney R.W.,
RA   Wines M., Hwang S., Bevins C.L.;
RT   "Enteric beta-defensin: molecular cloning and characterization of a
RT   gene with inducible intestinal epithelial cell expression associated
RT   with Cryptosporidium parvum infection.";
RL   Infect. Immun. 66:1045-1056(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96014297; PubMed=8589529;
RA   Gallagher D.S. Jr., Ryan A.M., Diamond G., Bevins C.L., Womack J.E.;
RT   "Somatic cell mapping of beta-defensin genes to cattle syntenic group
RT   U25 and fluorescence in situ localization to chromosome 27.";
RL   Mamm. Genome 6:554-556(1995).
CC   -!- FUNCTION: Has antibacterial activity (Potential).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Inducibly expressed in enteric epithelial
CC       cells.
CC   -!- SIMILARITY: Belongs to the beta-defensin family. LAP/TAP
CC       subfamily.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF000362; AAC48805.1; -.
DR   EMBL; AF016539; AAC48804.1; -.
DR   HSSP; P46170; 1BNB.
DR   InterPro; IPR001855; Defensin_beta.
DR   InterPro; IPR006080; Defensin_mammal.
DR   Pfam; PF00711; Defensin_beta; 1.
DR   SMART; SM00048; DEFSN; 1.
KW   Antibiotic; Signal.
FT   SIGNAL        1     26       BY SIMILARITY.
FT   CHAIN        27     64       ENTERIC BETA-DEFENSIN.
FT   DISULFID     31     60       BY SIMILARITY.
FT   DISULFID     38     53       BY SIMILARITY.
FT   DISULFID     43     61       BY SIMILARITY.
SQ   SEQUENCE   64 AA;  7126 MW;  7E8642AE6F7A6068 CRC64;

  Query Match             17.4%;  Score 66;  DB 1;  Length 64;
  Best Local Similarity   31.6%;  Pred. No. 0.22;
  Matches   18;  Conservative    7;  Mismatches   30;  Indels    2;  Gaps    2;

Qy          5 LLFAVFFCLVQRNSGDIPPGIRNTV-CFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              ||  : | ::   ||    || | : | : || |    |    |:   |  |  :||
Db          6 LLLTLLFLVLSAGSG-FTQGISNPLSCRLNRGICVPIRCPGNLRQIGTCFTPSVKCC 61


RESULT 14
D103_HUMAN
ID   D103_HUMAN     STANDARD;      PRT;    67 AA.
AC   P81534; Q9NPF6;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Beta-defensin 103 precursor (Beta-defensin 3) (DEFB-3) (BD-3) (hBD-3)
DE   (HBD3) (Defensin like protein).
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GN   DEFB103 OR DEFB3 OR BD3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., SEQUENCE OF 23-67, FUNCTION, TISSUE SPECIFICITY,
RP   INDUCTION, AND MASS SPECTROMETRY.
RC   TISSUE=Keratinocytes, Lung epithelial cells, and Tracheal epithelium;
RX   MEDLINE=21101950; PubMed=11085990;
RA   Harder J., Bartels J., Christophers E., Schroeder J.-M.;
RT   "Isolation and characterization of human deta-defensin-3, a novel
RT   human inducible peptide antibiotic.";
RL   J. Biol. Chem. 276:5707-5713(2001).
RN   [2]
RP   SEQUENCE FROM N.A., AND CHARACTERIZATION.
RX   MEDLINE=21558153; PubMed=11702237;
RA   Garcia J.-R., Jaumann F., Schulz S., Krause A., Rodriguez-Jimenez J.,
RA   Forssmann U., Adermann K., Kluver E., Vogelmeier C., Becker D.,
RA   Hedrich R., Forssmann W.-G., Bals R.;
RT   "Identification of a novel, multifunctional beta-defensin (human
RT   beta-defensin 3) with specific antimicrobial activity. Its
RT   interaction with plasma membranes of Xenopus oocytes and the
RT   induction of macrophage chemoattraction.";
RL   Cell Tissue Res. 306:257-264(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21125233; PubMed=11223260;
RA   Jia H.P., Schutte B.C., Schudy A., Linzmeier R., Guthmiller J.M.,
RA   Johnson G.K., Tack B.F., Mitros J.P., Rosenthal A., Ganz T.,
RA   McCray P.B. Jr.;
RT   "Discovery of new human defensins using a genomics-based approach.";
RL   Gene 263:211-218(2001).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Imai Y.;
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Adler D.A., Diamond G., Sheppard P., Holloway J., Presnell S.,
RA   Jaspers S., Whitmore T., Fox B., Gosink J., Rixon M., Gao Z.,
RA   Haldeman B., O'Hara P.;
RT   "EST and genomic database mining yield novel human and mouse
RT   beta-defensins.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   STRUCTURE BY NMR OF 23-67.
RX   MEDLINE=21864161; PubMed=11741980;
RA   Schibli D.J., Hunter H.N., Aseyev V., Starner T.D., Wiencek J.M.,
RA   McCray P.B. Jr., Tack B.F., Vogel H.J.;
RT   "The solution structures of the human beta-defensins lead to a better
RT   understanding of the potent bactericidal activity of HBD3 against
RT   Staphylococcus aureus.";
RL   J. Biol. Chem. 277:8279-8289(2002).
CC   -!- FUNCTION: Exhibits antimicrobial activity against Gram-positive
CC       bacteria S.aureus and S.pyogenes, Gram-negative bacteria
CC       P.aeruginosa and E.coli and the yeast C.albicans. Kills
CC       multiresistant S.aureus and vancomycin-resistent E.faecium. No
CC       significant hemolytic activity was observed.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highly expressed in skin and tonsils, and to a
CC       lesser extent in trachea, uterus, kidney, thymus, adenoid, pharynx
CC       and tongue. Low expression in salivary gland, bone marrow, colon,
CC       stomach, polyp and larynx. No expression in small intestine.
CC   -!- INDUCTION: By infection of bacteria and by interferon gamma.
CC   -!- MASS SPECTROMETRY: MW=5154.59; METHOD=Electrospray; RANGE=23-67.
CC   -!- SIMILARITY: Belongs to the beta-defensin family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ237673; CAC03097.1; -.
DR   EMBL; AF295370; AAG02237.1; -.
DR   EMBL; AF217245; AAF73853.1; -.
DR   EMBL; AB037972; BAB40572.1; -.
DR   EMBL; AF301470; AAG22030.1; -.
DR   PDB; 1KJ6; 20-MAR-02.
DR   Genew; HGNC:15967; DEFB103.
DR   MIM; 606611; -.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0008224; F:Gram-positive antibacterial peptide activity; TAS.
DR   GO; GO:0006965; P:anti-Gram-positive bacterial polypeptide in. . .; TAS.
DR   InterPro; IPR001855; Defensin_beta.
DR   Pfam; PF00711; Defensin_beta; 1.
KW   Antibiotic; Signal; 3D-structure.
FT   SIGNAL       1     22
FT   CHAIN       23     67       BETA-DEFENSIN 103.
FT   DISULFID     33     62
FT   DISULFID     40     55
FT   DISULFID     45     63
SQ   SEQUENCE   67 AA;  7697 MW;  54266DE1C90D4B65 CRC64;

  Query Match             17.4%;  Score 66;  DB 1;  Length 67;
  Best Local Similarity   31.7%;  Pred. No. 0.23;
  Matches   19;  Conservative    8;  Mismatches   27;  Indels    6;  Gaps    2;

Qy          5 LLFAVPFCLVQRNSGDIPPGIRNTV----CFMQRGHCRLFMCRSGERKGDICSDPWNRCC 60
              ||||: | :   |    || ||:    | :: | | :  |   | :   ||    :||
Db          6 LLFALLPLFLVPVPGH--GGIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCC 63


RESULT 15
DEF1_MACMU
ID   DEF1_MACMU     STANDARD;      PRT;    96 AA.
AC   P60030; P82318;
DT   15-MAR-2004 (Rel. 43, Created)
DT   15-MAR-2004 (Rel. 43, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Neutrophil defensin 1 precursor (RMAD-1).
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A., SEQUENCE OF 67-96, AND MASS SPECTROMETRY.
RC   TISSUE=Bone marrow, and Leukocyte;
RX   MEDLINE=20002603; PubMed=10531277;
RA   Tang Y.Q., Yuan J., Miller C.J., Selsted M.E.;
RT   "Isolation, characterization, cDNA cloning, and antimicrobial
RT   properties of two distinct subfamilies of alpha-defensins from rhesus
RT   macaque leukocytes.";
RL   Infect. Immun. 67:6139-6144(1999).
CC   -!- FUNCTION: Has bacteriostatic activity against Gram-positive
CC       bacteria S.aureus and L.monocytogenes and Gram-negative bacterium
CC       E.coli and antifungal activity against C.neoformans. Has
CC       microbicidial activity against Gram-positive bacteria S.aureus and
CC       L.monocytogenes.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- MASS SPECTROMETRY: MW=3446.9; METHOD=MALDI; RANGE=67-96.
CC   -!- SIMILARITY: Belongs to the corticostatin/defensin family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF188268; AAF06312.1; -.
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DR   PIR; A59076; A59076.
DR   HSSP; P11479; 1DFN.
DR   InterPro; IPR006081; Defensin_alpha.
DR   InterPro; IPR006080; Defensin_mammal.
DR   InterPro; IPR002366; Defensin_propep.
DR   Pfam; PF00323; defensins; 1.
DR   Pfam; PF00879; Defensin_propep; 1.
DR   SMART; SM00048; DEFSN; 1.
DR   PROSITE; PS00269; DEFENSIN; 1.
KW   Defensin; Antibiotic; Fungicide; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   PROPEP       20     66
FT   CHAIN        67     96       NEUTROPHIL DEFENSIN 1.
FT   DISULFID     68     95       BY SIMILARITY.
FT   DISULFID     70     85       BY SIMILARITY.
FT   DISULFID     75     96       BY SIMILARITY.
SQ   SEQUENCE   96 AA;  10544 MW;  BBC8A81AD8E304C5 CRC64;

  Query Match             17.3%;  Score 65.5;  DB 1;  Length 96;
  Best Local Similarity   35.6%;  Pred. No. 0.38;
  Matches   16;  Conservative    5;  Mismatches   15;  Indels    9;  Gaps    3;

Qy         20 DIPPGIR-NTVCFMQRGHCRLFMCRSGERKGDIC---SDPWNRCC 60
              |  ||:| |  |:     ||:  | :|||:   |      |  ||
Db         57 DSVPGLRKNMACY-----CRIPACLAGERRYGTCFYLGRVWAFCC 96


Search completed: June 14, 2004, 16:39:32
Job time : 15 secs
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